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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	JS-09-909-320-423	JS-09-905-291A-42	IS-09-902-853-423	JS-09-907-824-423	IS-09-907-841-423	-60-	-09-	-60-	-60-	-60-	JS-09-904-859-423	JS-09-909-204-423	JS-09-904-820-423	US-09-904-786-423
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US-09-906-646-423	US-09-906-700-423	903-	US-09-902-903-423	JS-09-903-749A-423	-4	US-09-904-956-423	-60	US-09-907-794-423	US-09-903-943-423	US-09-904-462-423	-106-60	-60	-60	US-09-905-056-423	US-09-909-064-423	US-09-904-553-423	US-09-905-381-423	US-09-905-088-423	18-09-907-575-423	US-09-905-075-423	US-09-902-759-423	US-09-902-634-423	US-09-902-713-423	US-09-907-979-423	US-09-902-615-423	US-09-903-925-423	US-09-906-760A-423	-09-903-823	US-09-907-652-423	
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## ALIGNMENTS

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
Sequence 423, Application US/09909320 Patent No. US20020132240A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                           Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary B.
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Mather, Jennie P.
                                                                               Ashkenazi, Avi
Botstein, David
                                                             APPLICANT: Genentech, Inc.
                                                                                                                                          Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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100.0%; Score 1637; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0;
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TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,088B

CURRENT FILING DATE: 2001-07-18

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PELING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

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PRIOR PILING DATE: 1999-11-29

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PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03

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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Williams, P. Mickey
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gao, Wei-Qiang
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100.0%; Pred. No. 2.1e-134;
iive 0; Mismatches 0;
PRIOR FULING DATE: 1939-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1939-07-26
PRIOR PLING DATE: 1939-07-26
PRIOR PLING DATE: 1939-07-28
PRIOR PLING DATE: 1939-09-08
PRIOR PLING DATE: 1939-09-08
PRIOR PLING DATE: 1939-09-13
PRIOR PLING DATE: 1939-09-13
PRIOR PLING DATE: 1939-09-15
PRIOR PLING DATE: 1939-10-15
PRIOR PLING DATE: 1939-10-29
PRIOR PLING DATE: 1939-11-29
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PRIOR PLING DATE: 1939-11-29
PRIOR PLING DATE: 1939-11-29
PRIOR PLING DATE: 1939-12-02
PRIOR PLING DATE: 1939-12-03
PRIOR PLING DATE: 2000-01-05
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Best Local Similarity 100.
Matches 310; Conservative
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; Pred. No. 2.1e-134;
0; Mismatches 0;
                                                                 PRIOR FULING DATE: 1999-015
PRIOR PELICATION NUMBER: PCT/US99/21089
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-30
     PILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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; Publication No. US2002019265941
; GENERAL INPORMATION:
; APPLICANT: Genentech, Inc.; APPLICANT: Botstein, David
; APPLICANT: Botstein, David
; APPLICANT: Betsein, David
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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Best Local Similarity 100.0%;
Matches 310; Conservative 0
                                                    FILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo Sapien
US-09-905-291A-423
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                                                                                                                                      121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                                                                                                           PIDSRANPRFRNSSFHLMSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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APPLICANT: Pan, James
APPLICANT: Pan, Micholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Workey
APPLICANT: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-8
PRIOR PILING DATE: 1999-07-8
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
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Grimaldi, Christopher J.
Grimaldi, Christopher J.
Hillan, Kemeth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Timas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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241 NIGGIIGGVLVVIAVLALITIGICCAYRRGYFINNKQDGESYRNPGKPDGVVYIRTDBEG 300
                              NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
NDRKEI DEI VI ELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary B.
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Hillan, Kenneth,
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
            Gerritsen, Mary B.
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APPLICANT: ROY, Margate Ann.
APPLICANT: Stewart, Timotby A.
APPLICANT: Stewart, Timotby A.
APPLICANT: Stewart, Timotby A.
APPLICANT: Timotby A.
APPLICANT: Timotby A.
APPLICANT: Timotby A.
APPLICANT: Wood, Williams, D. Wickey
APPLICANT: Wolliams, D. Wickey
TITLE OF INVENTION: Screeted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Acids Encoding the Same
PRIOR FILING DATE: 1090-02-22
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
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                                      Pan, James
Paoni, Nicholas F.
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US-09-907-841-423
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PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-30
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Sequence 421.42.

Publication No. US2002019836A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Bathenazi, Avi

APPLICANT: Betteth, David

APPLICANT: Baton, David

APPLICANT: Baton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerber, Hanspeter

APPLICANT: Gedber, Hanspeter

APPLICANT: Gedber, Hanspeter

APPLICANT: Gedberd, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Goddard, Paul J.

APPLICANT: Grimaldi, Christopher J.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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ORGANISM: Homo Sapien
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Length 310;

US-09-904-011-423; Sequence 423; Application US/09904011

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrar
ITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 99/665,350

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-18

PRIOR PELING DATE: 1999-09-18

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-09

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-16

PRIOR PELING DATE: 1999-12-16

PRIOR PELING DATE: 1999-12-20

PRIOR PELING DATE: 1999-12-20
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CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT PILING DATE: 2001-07-11
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Hublication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Estein, David
APPLICANT: Eston, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT:
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                                                                                           1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFBSVBLSCIITDSQT 60
                                                                                                                      1 MALRRPPRIRICARLPDFFILLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                Gaps
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Length 310;
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  100.0%; Score 1637; DB 10;
100.0%; Pred. No. 2.1e-134;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT PILLING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILLING DATE: 2000-09-18
PRIOR PILLING DATE: 2000-02-22
PRIOR PILLING DATE: 2000-02-22
PRIOR PILLING DATE: 1999-07-07
PRIOR PILLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILLING DATE: 1999-07-07
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Filvaroff, Blen
Fong, Sherman
Gao, Wei-Giang
Gerber, Hanspeter
Geritten, Mary E.
Goddard, A.
Godowski, Paul J.
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Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Stewart, Timothy A.
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Paoni, Nicholas P.
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Mather, Jennie P.
    Query Match
Best Local Similarity 100.
Matches 310; Conservative
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Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
                                   Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                             Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                  Fong, Sherman
Gao, Wei-Oiang
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US-09-906-838-423
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Best Local Similarity
Matches 310; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 NIGGIIGGVLVVIAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 NIGGIIGGVLVVIAVLALITIGICCAYRRGYFINNKQDGBSYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120
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PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
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PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
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PRIOR PILING DATE: 1999-12-07
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PRIOR PILING DATE: 1999-12-07
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Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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ORGANISM: Homo Sapien
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US-09-907-613-423
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APPLICANT:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timcthy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT PILING DATE: 2001-07-17
REIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
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                                                                                         61 SDPRIEWKKIQDEQTITVFFDNKIQGDLAGRARILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                                                                                                            241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                   9
121 NDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
                                                                                                                                                                                                                                   181 PIDSRANPRFRNSSFHLNSETGILVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
                                                                      SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Bilen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerriteen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-907-613-423
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61 SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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; Pred. No. 2.1e-134;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NOS: 423
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Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
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Eaton, Dan L.
Perrara, Napoleone
Pilvaroff, Ellen
Pong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 100.
Matches 310, Conservative
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301 DFRHKSSFVI 310
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ORGANISM: Homo Sapien
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NDRKEI DEIVIELTVQVKPVTPVCRVPKAVPVGRMATLHCQESEGHPRPHYSWYRNDVPL
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Gerritsen, Mary E.
Goddard, A.
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Hillan, Kenneth,
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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100.0%; Score 1637; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            THILK BERENGUE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,942

CURRENT PILIAG DATE: 2002-01-22

CURRENT PILIAG DATE: 2002-01-22

PRIOR APPLICATION NUMBER: PCT/US00/04114

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-06

PRIOR PLING DATE: 1999-10-06

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-06

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PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-07
                    Goddard, A.
Goddwski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Gerritsen, Mary E.
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SEQ ID NO 423
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TYPE: PRT
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241 NIGGIIGGYLVVLAVLALITIKJICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 300
241 NIGGIIGGYLVVLAVLALITIGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                  181 PTDSRANPRPRISSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
                                                                                                   PTDSRANPRFRNSSFHIASETGTLVFTAVHKDDSGQYYCIASNDAGSARCERQEMBVYDL
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APPLICANT: Milan, Kenneth, J.
APPLICANT: Milavin, Ivar J.
APPLICANT: Milavin, Ivar J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: WINGER: U6466-14
CURRENT APPLICATION NUMBER: U5/09/904,859
PRIOR APPLICATION NUMBER: U5 60/145,698
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-03
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Publication No. US20030036060A1
GENERAL INFORMATION:
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APPLICANT: ROY, MANGENIA F.
APPLICANT: ROY, MANGENIA F.
APPLICANT: Severt, Timchy A.
APPLICANT: Severt, Timchy A.
APPLICANT: Severt, Timchy A.
APPLICANT: Severt, Timchy A.
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, I.
ITITE OF INVENTIOR: Secreted and Transmembrane Polypeptides and Mucleic TITIE OF INVENTIOR: 10466-14
CURRENT FALLIAN DATE: 2001-07-18
FRIOR PELLON NOWER: 1050-00-02-25
FRIOR PELLON NOWER: 1050-00-02-25
FRIOR PELLON WORE: 1050-00-02-25
FRIOR PELLON WORE: 1050-00-15
FRIOR APPLICATION WORE: PCT/US99/2034
FRIOR PELLON WORE: 1050-00-15
FRIOR APPLICATION WORE: PCT/US99/2034
FRIOR PELLON FRIE 1050-00-15
FRIOR APPLICATION WORE: PCT/US99/2034
FRIOR APPLICATION WORE: PCT/US99/2031
FRIOR PELLON WORE: 1959-10-05
FRIOR APPLICATION WORE: PCT/US99/2031
FRIOR PELLON WORE: PCT/US99/2031
FRIOR PELLON WORE: PCT/US99/2035
FRIOR PELLON WORE: PCT/US99/2039
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          Mather, Jennie P.
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; ORGANISM: Homo Sapien
US-09-909-204-423
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2.1e-134;
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-05
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
ELENGTH: 310
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Fublication No. US20030036061A1
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Blien
APPLICANT: Fivaroff, Blien
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gerritsen, Mary E.
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US-09-909-204-423
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Length 310; Indels

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121 NDRKEIDEIVIELITVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSMYRNDVPL 180
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
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Gao, Wail-Olang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
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Kljavin, Ivar J.
Mather, Jennie P.
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Ferrara, Napoleone
Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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ORGANISM: Homo Sapien
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APPLICANT:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Timochy A.
APPLICANT: William, P. Wickey
APPLICANT: Wood, William, 1.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Societies 2001-07-13
PRIOR PELICATION NUMBER: US/09/65,350
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 1999-00-22
PRIOR PELING DATE: 1999-00-22
PRIOR PELING DATE: 1999-00-30
PRIOR PELING DATE: 1999-00-30
PRIOR PELING DATE: 1999-00-13
PRIOR PELING DATE: 1999-00-13
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20190
PRIOR APPLICATION NUMBER: PCT/US99/20190
PRIOR APPLICATION NUMBER: PCT/US99/20190
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-00
PRIOR PELING DATE: 1999-12-02
                           RESULT 14
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Betstein, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Besnoyers, Luc
; APPLICANT: Raton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                           Perrara, Napoleone
Filvaroff, Bllen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
Goddard, A.
                                                                                                                                               301 DFRHKSSFVI 310
                                                                                                               301 DFRHKSSFVI 310
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDPRIEWKKIODEQTTYVPPDNKIQGDLAGRAEILGKTSLKIMNVTRRDSALYRCEVVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDPRIEWRKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALRRPPRLETCARLPDFFLLLFRGCLIGAVNLKSSNRTPVVQEFESVBLSCIITDSQT 60
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT PRIJING DATE: 2001-07-12
FRIOR PILING DATE: 2001-07-18
FRIOR PILING DATE: 2000-09-18
FRIOR PILING DATE: 2000-09-18
FRIOR PILING DATE: 2000-09-18
FRIOR PILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVBLSCIITDSQT
                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 310; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 DFRHKSSFVI 310
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Search completed: June 15, 2004, 11:08:02 Job time: 40 secs

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OM protein - protein search, using sw model

Run on:

June 15, 2004, 10:59:09; Search time 14.5 Seconds (without alignments) 2056.508 Million cell updates/sec

US-09-524-531C-15 score:

1 MALRRPPRIRICARLPDFFL...................310

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR 78:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length DB	90	O.	Description
				!		
-	424	25.9	299	~	S56749	onal a
7	187	11.4	725	N	JE0099	
٣	186	11.4	1088	<del>, -1</del>	ICKINI	neural cell adhesi
4	180.5	11.0	1894	N	C54689	protein-tyrosine-p
ហ	177	10.8	725	~	JE0100	neural cell adhesi
9	177	10.8	1092	Н	JN0635	
7	174	10.6	333	7	A31923	⋍
80	171.5	10.5	725	-	IJMSNG	
O	171.5	10.5	1115	Н	IJMSNI	cell
10	169.5	10.4	858	Н	LJRTNC	neural cell adhesi
11	169.5	10.4	1912	~	A56178	protein-tyrosine-p
12	164.5	10.0	3707	7	S18252	heparan sulfate pr
13	163.5	10.0	1051	7	A39712	kinase-like protei
14	161.5	9.6	853	ч	IJBONC	neural cell adhesi
15	191	9.6	538	~	JC2457	ır cel
16	191	9.8	1001	Н	LJCHNL	cel1
17	160.5	9.6	761	Н	IJHONG	neural cell adhesi
18	160.5	9.6	1612	N	T30805	•
19	160	9.8	7962	7	I38346	elastic titin - hu
20	159.5	9.7	1033	~	S19247	cell adhesion prot
21	159.5	9.7	6642	N	T29757	
22	159	9.7	1323	N	PN0568	connectin 3B - chi
23	159	7.6	4162	~	T42633	connectin/titin -
24	155.5	9.5	1259	~	A43425	~
25	155.5	9.5	1268	-	A39640	neural cell adhesi
26	155	9.5	344	~	156551	neurotrimin - rat
27	155	9.5	1907	7	S50893	protein-tyrosine-p
28	154.5	9.4	495	7	T25750	hypothetical prote
29	154	9.4	1501	7	158148	protein-tyrosine-p

protein-tyrosine-p hypothetical prote	hypothetical prote hypothetical prote	coxgackie- and ade carcinoembryonic a	transmembrane rece	billary glycoprote	protein-tyrosine-p	protein-tyrosine k	protein-tyrosine k	leukocyte antigen-	leukocyte antigen-	hypothetical prote	biliary glycoprote
S46217 T33433	T33434 T17346	JC7780 A36319	T14160	S34338 B48758	A48758	148696	148697	TDHULK	846216	T29549	JC1509
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1863	875 483	365	1651	521	1496	871	881	1897	1898	423	458
0. 0.	0 0 0 0	0 0	9.5	90	0.0	9.0	9.0	9.0	9.0	8.9	8.9
154	153	150.5	150	149	148	147.5	147.5	147.5	147	146.5	146.5
30	33	3.4	36	37	3 6	40	41	42	43	44	45

# ALIGNMENTS

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		6
3	49	5
3	4	1

junctional adhesion molecule precursor - human N;Alternate names: P11 platelet antigen; platelet adhesion molecule PAM-1; platelet P11

A; Molecule type: protein A;Residues: 28-49,'X',51-53;62-73,'B',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X A;Note: the order of the peptides other than the amino terminus was not determined

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #esquence\_revision 01-Feb-2002 #text\_change 01-Feb-2002
C;Accession: A59406; S56749
R;Ozaki, H; Ishli, K; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut
A;Reference number: A59406; MUD:99323940; PMID:10395639
A;Reference pye: DNA
A;Residue: preliminary
A;Molecule type: DNA
A;Residue: 1-299 coZa>
A;Cross-references: GB:AAD42050; NID:95326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
B;Cross-references: GB:AAD42050; MUD:95374438; PMID:7646439
A;Reference number: S56749; MUD:95374438; PMID:7646439
A;Accession: S56749

C.Genetics:

A;Gene: JAM C;Keyworda: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane P;1-25/Domain: signal sequence #status predicted <SIG> F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Gape 22; Query Match
25.9%; Score 424; DB 2; Length 299;
Best Local Similarity 32.8%; Pred. No. 1.4e-27;
Matches 101; Conservative 48; Mismatches 137; Indels

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KKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIMNVTRRDSALYRCEVVARNDRKEID 127 68

63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSBEGGNSYG 120 ò 엄

128 RIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187 ठे

188 PRFRNSSFHINSBTGTLVFTAVHXDDSGQYYCIASNDAGSARCBEQ-EMBVYDLNIGGII 121 a ð

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247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDERGDF 302  rm #status predicted <I domain form #status pr

17

**Gaps** 

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F.20-803,1050-1088 Product: neural cell addression molecule, short domain form flatatus predicted (BXT)-
F.20-705/Domain: extracellular flatatus predicted (BXT)-
F.34-95/Domain: mamunoglobulin homology (MMM)-
F.3129-188/Domain: immunoglobulin homology (MMM)-
F.3129-188/Domain: immunoglobulin homology (FMM)-
F.313-184/Domain: immunoglobulin homology (FMM)-
F.317-384/Domain: immunoglobulin homology (FMM)-
F.317-384/Domain: immunoglobulin homology (FMM)-
F.317-389/Domain: immunoglobulin homology (FMM)-
F.317-380/Domain: immunoglobulin homology (FMM)-
F.317-380/Domain: immunoglobulin homology (FMM)-
F.317-380/Domain: immunoglobulin homology (FMM)-
F.317-380/Domain: immunoglobulin homology (FMM)-
F.318-1886/Domain: intransmembrane flatatus predicted (IMM)-
F.319,310,341,417,443,472/Binding site: carbohydrate (ABN) (covalent) flatatus predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKBIDBIV-IELTVQV 137
long domain form #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GAVNIK-----SSNRTPVVQBFESVBLSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 11.4%; Score 186; DB 1; Similarity 28.9%; Pred. No. 3.2e-07; 61; Conservative 30; Mismatches 84
            cell adhesion molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
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A;Molecule type: mRNA
A;Residues: 1-1894 eMIZ>
A;Experimental Source: brain; splice form B
A;Note: sequence inconsistent with nucleotide
A;Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 NEDQSEWITHHVEKDDEABYSCIANNQAGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 61; Conserv
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JED099
neural cell adhesion molecule 1 - African clawed frog
NiAlternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Dete: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
R;Kudo, M: Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Ritle: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMS) as the mata; Residues: 1-725 Kudo)
A;Rocession: JE0099
A;Molecule type: mRND
A;Residues: 1-725 Kudo)
A;Rosidues: 1-725 Kudo)
A;Cross-references: DDBJ:AB008162; NID:G3116226; PIDN:BAA25931.1; PID:G3116227
A;Rosidues: 1-725 Kudo)
A;Ryperimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bc
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
P;413-475/Domain: immunoglobulin homology <1MM>
P;512-589/Domain: fibronectin type III repeat homology <1RM>
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NiAlternate names: NCAM-180

NiAlternate names: NCAM-180

NiContains: neural cell adhesion molecule, short domain form (NCAM-140)

Cispecies: Xenopus laevis (African clawed frog)

C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C; Accession: S09600

R; Xitieg, P.-A.: Sakaguchi, D.S.; Kintner, C.R.

Nucleic Acids Res. 17, 10321-10335, 1989

A; Title: Primary structure and developmental expression of a large cytoplasmic domain fc

A; Accession: S09600; MUID: 90098871; PMID: 2481269

A; Accession: S09600

A; Molecule type: mRNA

A; Residues: 1-1088 «KRI»

A; Cross-references: EMBL: M25696; NID: 9214609; PIDN: AA49909.1; PID: 9214610

A; Note: the authors translated the codon AAA for residue 970 as Leu

C; Comment: Several forms of NCAM are produced by alternative splicing.

C; Genetics:

A; Gene: NCAM

C; Genetics:

A; Gene: NCAM

C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C; Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; sil

P; 1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ξÇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neural cell adhesion molecule long domain form precursor - African clawed frog
            --- ARSEGEP 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 28.9%; Pred. No. 1.6e-07; 61; Conservative 30; Mismatches 84;
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                                                                                             303 RHKSSFVI 310
                                                                                                                                        : |||::
292 KQTSSFLV 299
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Best Local S:
Matches 61
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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor NyAlternate names: MPTP delta type B/C
NyAlternate names: MPTP delta type B/C
NyContains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C54689; B54689
C;Accession: C54689; B54689
Mol: Call Biol: 13, 5513-5523, 1993
A;Fitle: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specializ A;Reference number: A54689; MUID:93360986; PMID:8355697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hy F;45-107/Domain: immunoglobulin homology <IMM1> F;245-299/Domain: immunoglobulin homology <IMM2> F;245-299/Domain: immunoglobulin homology <IMM2> F;317-399/Domain: fibronectin type III repeat homology <FN3A> F;218-1894/Domain: leukocyte common antigen cytosolic domain homology <IAC> F;1278-1894/Domain: protein-tyrosine-phosphatase homology <PTP2> F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: brain; splice form C
A; Note: sequence inconsistent with nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C; Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                         138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHL 197
160 DV-----RFVVILANNYLQIRGIKKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation (NCBIN:137487)
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A;Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
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A; Accession: A31923
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JB0100
Incural cell adhesion molecule 2 - African clawed frog
Incural cell adhesion molecule 2 - African clawed frog
N;Alternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0100
R;Xudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem: Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the mata Richem on the cloude type: mRNA
A;Reference number: JE0100
A;Accession: JE0100
A;Accession: JE0100
A;Accession: JE0100
A;Residues: 1-725 - KUD>
A;Accession: Jeologan and regulates various cell-cell interactions through bc C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu F;413-475/Domain: immunoglobulin homology <IMM>F;512-589/Domain: fibronectin type III repeat homology <JRM>F;512-589/Domain: fibronectin type III repeat homology <JRM>F;512-589/Domain: fibronectin type III repeat homology <JRM>F;512-589/Domain: fibronectin type III repeat homology 
                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                     57 DSQTSDPR--IEW----KKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIMNVTRRDS 110
                                                                                                                                                                                                                                                                                                                111 ALYRCEVVARNDRKBIDBIVIELTVQVKPVTPVCRVPKAVPVGKM------ATL 158
                                                                                                                                                                                                                                                                                                                                                                                                              153 LCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSESIGALQIEQSEESDQGKY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 GTVNLKIYQKLTPKYAPTPQEPTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 KIQGDLAGRABILGKTSLKIWNVTRRDSALYRCB--VVARNDRKBIDBIVIELTVQVKPV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 DV-----RFVVLANNYLQIRGIKKTDEGAYRCEGRILARG---EINYKDIQVIVAVPPL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 TPV--CRVPKAVPVGKMATLHCORSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLN 198
                                                                                                                                                                                             26
                                                                                                                                                                                                                                       11 VRRPLSLLITPFLCACAETPPRP------TRTPVDQTGVSGGVASPIC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 HCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSET-GTLVFTAVHKDDSGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 GAVNLKSSNR-----TPVVQBFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN
                                                                                                                                                                                        3 LRRPPRLRL-----CARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIIT
                                                                                                                                              Gaps
                   #status predicted predicted
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                                                                                               Length 1894;
    predicted
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28.6%; Pred. No. 1.1e-06;
ive 28; Mismatches 88; Indels
F:1542/Binding site: substrate phosphate (Arg) #status F:1826/Active site: Cys (phosphocysteine intermediate) F:1832/Binding site: substrate phosphate (Arg) #status
                                                                                          Query Match 11.0%; Score 180.5; DB 2; Best Local Similarity 28.8%; Pred. No. 1.8e-06; Matches 72; Conservative 34; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 28.6
Matches 60; Conservative
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C;Species: Xenopus laevis (African clawed frog)
C;Species: Name 1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
R;Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993
A;Title: Two neural-cell adhesion molecule (NCAM) -encoding genes in Xenopus laevis are e A;Reference number: JN0635
A;Reference number: JN0635
A;Accession: JN0635
A;Accession: JN0635
A;Accession: JN0635
A;Accession: JN0635
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A;Accession: JN0635
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Cybener NCAW2

Cybener NCAW2

Cybener Special adhesion molecule; fibronectin type III repeat homology; imm

Cybeywords: alternative splicing; cell adhesion; duplication; heparin binding; sialogly

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
F;20-105/Domain: extracellular #status predicted <SXT>
F;30-705/Domain: extracellular #status predicted
F;34-95/Domain: immunoglobulin homology <IPM1>
F;129-188/Domain: immunoglobulin homology <IPM2>
F;149-157/Region: heparin binding #status predicted
F;149-157/Region: heparin binding #status predicted
F;141-157/Domain: immunoglobulin homology <IPM3>
F;141-157/Domain: fibronectin type III repeat homology <FN3A>
F;121-589/Domain: fibronectin type III repeat homology <FN3A>
F;121-589/Domain: fibronectin type III repeat homology <FN3A>
F;120-780/Domain: fibronectin type III repeat homology <FN3A>
F;120-780/FN3A
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F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Drosophila melanogaster
C;Species: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1092 <TON>
A;Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc
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ural cell adhesion molecule 2 precursor - African clawed frog
Species: Xenopus laevis (African clawed frog)
Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
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Best Local Similarity
Matches 60; Conserv
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A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921 A; Molecule type: DNA A; Residues: 1-333 <SEE>

A,Gene: PlyBase:Ama A,Cross-references: FlyBase:FBgn0000071

Query Match

Score 174; DB 2; Length 333; 10.6%; us-09-524-531c-15.rpr

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Pred. No. 3.1e-06;
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A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
   27.3%;
                            63; Conservative
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Best Local Similarity
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C:Species: Nue musculus (house mouse)
C:Date: 1.-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S0382; A44290
R:Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec EMBO J. 6, 907-914, 1987
A:Pitle: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00d
A:Pitle: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00d
A:Pitle: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00d
A:Pitle: Isolation and nucleotide sequence of mouse NCAM CDNA that Codes for a Mr 79,00d
A:Pitle: Differences: EMBL: YOUS5; NID:G53342; PMID:359563
A:Pitle: Differences: EMBL:YOUS5; NID:G53342; PMID:359563.1; PID:G53343
A:Pitle: Differences: EMBL:YOUS5; NID:G53342; PMID:3396534
A:Pitle: Differences: DNA
A:Pitle: Differences: DNA
A:Pitle: Structural and immunological characterization of the amino-terminal domain of mark A:Pitle: Structural and immunological characterization of the amino-terminal domain of mark A:Residues: 20-36 A:ROUS
C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mediates coloment: Several forms of NCAM are produced by alternative splicing. See also PIR:IUMS
C:Comment: Several forms of NCAM are produced by alternative splicing.
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A,Map position: 9
A,IMap position: 9
A,IMap position: 9
A,Introns: 701/1
C,Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C,Superfamily: neural sequence #status predicted <81G>
F,1-19/Domain: signal sequence #status predicted <81G>
F,1-19/Domain: immunoglobulin homology <IVM1>
F;132-191/Domain: immunoglobulin homology <IVM2>
F;152-191/Domain: immunoglobulin homology <IVM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IVM3>
F;23-388/Domain: immunoglobulin homology <IVM4>
F;23-388/Domain: immunoglobulin homology <IVM4>
F;20-482/Domain: immunoglobulin homology <IVM4>
F;20-596/Domain: immunoglobulin homology <IVM4>
F;21-596/Domain: immunoglobulin homology <IVM4>
F;21-596/Domain: fibronectin type III repeat homology <FN3B>
F;21-596/Domain: fibronectin type III repeat homology <FN3B>
F;21-61-61,13-189;235-288;330-386;427-480/Disulfide bonds: #status predicted
F;22,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                       LGKTSLKIWNVTRRDSALYRCEVVARNDRKBIDBIVIELTVQVKPVTPVCRVPKAVPVGK 154
                                                                                                                                                                                                                                                                                                                                    MATLHCORSEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSPHLNSETGTLVFTAVHKDDS 214
                                                                                                                                                                                                                                                                                                                                                                          246 SAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGREDF 302
                                                                                             94
                                                                                             35 KSSNRTPVVQEPESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFPDNKIQGDLAGRAEI
                                   20; Gaps
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                                   Indels
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   26.3%; Pred. No. 7.7e-07;
                                51; Conservative 39; Mismatches
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   Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-580, TT, 550-571, TT, 553-574, DD, 576-588, MQPS', 593,'S', 595-599,'P',601,'1
A; Cross-references: EMBL:Y00051; NID:953342; PIDN:CDA68263.1; PID:953343
R; Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
Risantoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
Risantoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.;
A; Title: Analysis of CDNA clones that code for the transmembrane forms of the mouse nen
A; Reference number: S00844; MUID:88067687; PMID:3684567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: NCAM-180
NiContains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 31-Dec-2000
C;Accession: A29673; S00844; $00384; A28281; A44290; S00383
C;Accession: A29673; S00844; $00384; A28281; A44290; C; Chaix, J.C.; Hirsch, M.R.; Fonts EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00
A;Reference number: A29673; MUID:87246524; PMID:359553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: DNA
A, Residues: 642-1115 (SBR)-
A, Cross-references: BNBL:X07195
R, Barthels, D.; Vopper, G.; Wille, W.
Nuclaic Asida Res. 16, 4217-4225, 1980
A, Title: NCAW-180, the large isoform of the neural cell adhesion molecule of the mouse,
A, Reference number: A28281; MUID:88247737; PMID:2454455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mc; Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: mRNA
A.Residues: 529-809,1077-1115 cSAN>
A.Cross-references: BMBL:X06328; NID:953322; PIDN:CAA29641.1; PID:9817984
A.Cross-references: BMBL:X06328; NID:953322; PIDN:CAA29641.1; PID:9817984
R.Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
R.Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
A.Farbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
A.Farbas, J.A.; Steinmetz, Steinmetz, M.; Goridis, PMID:3396534
A.Reference number: S00382; MUID:88283628; PMID:3396534
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D. Biol. Chiem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of A;Reference number: A44290; MUID:86140120; PMID:3512556
12;
                                                                                                                                                               96 CVVTAEDGTQSEATVAVKIPQKLMPKNAPTPQBPKEGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                                                                                                                                                                             203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGPPEPTMSWTKDGRPIENEEB-D 260
                                                                                                                                                                                                                                                                                          72 DEQITYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDBI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                 CLIGA------VNLKSSNR-----TPVVQEPESVELSCIITDSQTS-DPRIEWKKIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOJecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: RMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 ERSRSSV----SDSSEVTIRNVDXNDEAEYVCIAENKAG-----EQDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRFRNSSFHINSETGTLVFTAVHXDDSGQYYCIASNDAGSARCEBQEMEVY 238
     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neural cell adhesion molecule 1 precursor, long domain splice form
     Indels
          41; Mismatches
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C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C;Feywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si P;10-115/Pomain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi P;20-8109,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta P;20-711/Domain: extracellular #status predicted <EXT>
F;24-88/Domain: extracellular #status predicted <EXT>
F;132-119/Domain: immunoglobulin homology <IRM1>
F;132-115/Fregion: heparin binding #status predicted F;161-165/Region: heparin binding #status predicted F;262-127/Region: heparin binding #status predicted F;262-27/Region: nCAM binding #status predicted F;262-28/Domain: immunoglobulin homology <IRM3>
F;262-27/Region: NCAM binding #status predicted F;313-388/Domain: immunoglobulin homology <IRM4>
F;262-28/Domain: immunoglobulin homology <IRM4>
F;262-68/Domain: immunoglobulin homology <IRM4>
F;262-68/Domain: immunoglobulin homology <IRM5>
F;265-68/Domain: immunoglobulin homology <IRM5>
F;275-68/Domain: immunoglobulin homology <IRM5>
F;275-68/Domain: immunoglobulin homology <IRM5>
F;275-68/Domain: intracellular #status predicted <IRM5>
F;275-68/Domain: intracellular #status predicted <IRM5-F;319-189,235-288,330-386,427-480/bisulfide bonds: #status predicted
F;41-96,139-189,235-288,330-386,427-480/bisulfide bonds: #status predicted
F;41-96,139-189,235-288,330-386,427-480/bisulfide bonds: #status predicted
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A; Molecule type: mRNA
A; Residues: 1.458 < SMA>
A; Cross_references: EMBL:X06564
B; Small, S.J.; Akeson, R.
A; Cfl Biol. 111, 2089-2096, 1990
A; Title: Expression of the unique NCAM VASB exon is independently regulated in distinct A; Reference number: A37795; MUID:91035620; PMID:1699951
A; Accession: B37795
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 340-381 < SM2>
B; Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A; Artile: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev A; Reference number: 158136; MUID:90166485; PMID:2483093
A; Accession: 158136
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-59-1991 #sequence revision 30-5ep-1991 #text_change 22-Jun-1999
C;Date: 30-59-1991 #sequence revision 30-5ep-1991 #text_change 22-Jun-1999
C;Date: 30-59-1991 #sequence revision 30-5ep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; ISB31
D; Call Biol. 105, 233-52345, 1987
D; Call Biol. 105, 233-52345, 1987
A;Ritle: Identification of a cDNA clone that contains the complete coding sequence for A;Reference number: S00846; MUID:88059265; PMID:3680385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 DEQTTYVPFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCE--VVARNDRKBIDBI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLIGA-----VNLKSSNR-----TPVVQEFBSVBLSCIITDSQTS-DPRIEWKKIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERSRSSV----SDSSEVTIRNVDXNDEABYVCIAENKAG-----EQDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCERQEMEVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 10.5%; Score 171.5; DB 1; Length 1 Local Similarity 27.3%; Pred. No. 5.2e-06; nes 63; Conservative 41; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
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AjGene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm
C;Superfamily: neural cell adhesion molecule adhesion; duplication; heparin binding; e
F;E-195/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <N
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                         7:31-30 Domain: immunoglobulin homology < IRMI2>
F:131-191/Domain: immunoglobulin homology < IRMI2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:263-278/Region: immunoglobulin homology < IRMI3>
F:263-278/Region: NCAM binding #status predicted
F:232-398/Domain: immunoglobulin homology < IRMI3>
F:253-606/Domain: immunoglobulin homology < IRMI3>
F:252-606/Domain: fibronectin type III repeat homology < FN3B>
F:722-739/Domain: transmembrane #status predicted < IRMI>
F:740-858/Domain: intracellular #status predicted < IRMI>
F:740-864,339-336-336,330-336,437-490/Disdifide bonds: #status predicted
F:741-864,139-189,235-288,330-396,437-490/Disdifide bonds: #status predicted
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A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644 C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mcC;Comment: Various forms of NCAM are produced by alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 390-1912 <KRU>
A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A;Note: the sequence from Pig. 5B is inconsistent with that from Pig. 5A in having 568-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CVVTAEDGTQSRATVNVKIFQKIMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
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A;Molecule type: mRNA
A;Residues: 1-1912 <PUL.
A;Cross-references: GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
R;Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 PRPRNSSPHL-NSBTGTLVPTAVHXDDSGQYYCIASNDAGSARCBGQBMBVY 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
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A;Reference number: A56178; MUID:95204468; PMID:7896816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 10.4%; Score 169.5; DB 1; il Similarity 26.3%; Pred. No. 5.6e-06; 61; Conservative 42; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 61; Conserv
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A;Molecule type: mRNA
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40 TPVVQEPESVE-----LSCIITDSQTSDPRIEWKKIQDEQTTYVFPDNKIQGDLAGRAE
      A; Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C: Keywords: ATP
P:775-1046/Doman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 66
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518252
heparam sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
S;Sullo: Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogla A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Recession: S18352
A;Molecule type: mRNA
A;References: EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
A;Cross-references: EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
A;Cross-references: EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
A;Cross-references: EMBL:M77174; NID:9200295; PIDN:AAA39911.1; PID:9200296
A;Title: Identification of coNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yad Cancer Res. 52, 737-740, 1992
A;Title: Protein-tyrobine phosphatase expression in pre-B cell NALM-6.
A;Reference number: A44929; MUID:92119637; PMID:1370651
A;Accession: B44929
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1756-1804, C, 1806-1845 <ADA>
A;Cross-references: GB:S78086; NID:9243545; PIDN:AAB21147.1; PID:9243546
A;Experimental source: pre-B cell NALM-6
A;Mote: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gy

C.Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F;38-100/Domain: immunoglobulin homology <IPML>

F;38-100/Domain: immunoglobulin homology <IPML>

F;360-304/Domain: immunoglobulin homology <IPML>

F;250-304/Domain: immunoglobulin homology <IPML>

F;250-304/Domain: immunoglobulin homology <IPMS>

F;151-30-304/Domain: ibronectin type III repeat homology <3FR>

F;120-304/Domain: perotein-type III repeat homology <PRP2>

F;120-304/Domain: protein-tyrosine-phosphatase homology <PRP2>

F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1859/Binding site: substrate phosphate (Arg) #status predicted

F;1850/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 9p24-9p24
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 BILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDBIVIELTVQVKPVTPVCRVPKAVPV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ATLACOESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTPVVQEFESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVPFDNKIQGDLAGRA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1912,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 T-----GTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMEVYDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGGTPIRGALQIEQSEESDQGKYBCVATNSAGTRYSAPANLYVREL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%; Score 169.5; DB 2;
28.6%; Pred. No. 1.5e-05;
M.smatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:131384; OMIM:601598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A31917
A; Molecule type: mRNA
A; Residues: 940-1601 <NO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       A, Gene: GDB: PTPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33
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A. Residues: 1272-1274, X', 1276, X', 1278-1279 <SGH>
C. Superfamily: LDL receptor ligand-binding repeat homology <LDL1>
F. 199-234/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F. 1985-319/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F. 1985-319/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F. 1888-403/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F. 1889-1206/Domain: LDL receptor ligand-binding repeat homology <LBG7>
F. 1881-1206/Domain: laminin-type EGF-like homology <LBG7>
F. 1891-1606/Domain: laminin-type EGF-like homology <LBG7>
F. 1815-1619/Domain: Baninin-type EGF-like homology <LBG8>
F. 1816-3198/Domain: Baninin-type EGF-like homology <LBG9>
F. 1816-3198/Domain: Baninin-type EGF-like homology
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A;Title: Characterization of a member of the immunoglobulin gene superfamily that possi
A;Reference number: A39712; MUID:91271300; PMID:1711213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: TIO51 (CHO)
A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
P,3464-3492/Domain: EGF homology < EGF7>
P,1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2428 LSVHGPPTVSV---LPB------GPVHVKMG-------KDITLECISSGEPR 2463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2510 NALGTAQKQV-ELIVD-TGTVAPGTPQVQVEESELTLEAGHTATLHC-SATGNPPPTIHW 2566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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C;Species: Gallus gallus (chicken)
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C;Accession: A39712
R;Chou, Y.H.; Hayman, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2464 SSPR--W------TRLGIPVKLEPRMFGLMN--SHAMLKLASVKPSDAGTYVCQ--AQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFBSVELSCIITDSQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P,3270-3423/Domain: laminin G repeat homology <LG2>
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P;783-791/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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C;Accession: JC2457
R;Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
Biochem Biophys. Res. Commun. 201, 805-812, 1 34
A;Title: Cloning and expression kinetics of po cine vascular cell adhesion molecule.
A;Reference number: JC2457; MUID:94271236; PMI :7516159
A;Accession: JC2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: JC245/
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Roscides: 1-538 <TSA-
A;Cross-references: BMBL: U08351; NID: 9474382; . IDN:AAA21542.1; PID: 9474383
A;Cross-references: BMBL: U08351; NID: 9474382; . IDN:AAA21542.1; PID: 9474383
C;Keywords: glycoprotein; transmembrane #status predicted
F;497-517/Domain: transmembrane #status predicted
F;75,157,271,330,360/Binding site: carbohydrat. (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                  130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : | | | | | | : | | | | : | | | | | : | | | | | | | : | | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                            96 CVVTAEDGTESEATVAVKIFQKLAFKAAPTPQEFREGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                           DEQTIYVFFDUKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-NAEGPPEPTVSWTKDGEQIENE--- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 GKTSLKIWNYTRRDSALYRÇEVV--ARNDRKE: DEIVIELTVQVKP--VTPVCRVPKAVP 151
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----VNLKSSNR-----TPVVQEFBSVBLSCIITDSQTS-DPRIBWKKIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vascular cell adhesion protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb_1995 #sequence_revision 05-Apr-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 PRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEGGEMEVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NALernate names: NCAM-140
N/Alternate names: NCAM-140
Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus
C;Species: J-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
R;ES Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and A;Reference number: A32976; MUID:89378239; PMID:2776887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 20-16 <RQU>
A; Residues: 20-36 <RQU>
A; Residues: 20-36 <RQU>
A; Note: 23-361u was also found
C; Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C; Comment: NCAM mediates cell-cell adhesion molecule; fibronectin type III repeat homology; immu
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C; Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
P; 1-19/Domain: signal sequence #status predicted <SIo>
F; 0-85, Product: neural cell adhesion molecule, short domain form #status experimental
F; 20-719/Domain: extracellular #status predicted <EXT>
F; 34-98/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figgraphy Commain: immunoglobulin homology activity
Figgraphy Commain: intransmembrane flatatus predicted activity
Figgraphy Commain: intracellular flatatus flatatus
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A.Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A.Note: the authors identified this protein as calmodulin-independent adenylate cyclase
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J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of A;Reference number: A44290; MUID:86140120; PMID:3512556
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                                                                                                                                                                                                                                           154 KWATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSBTGTLVPTAVHKDD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : : | | : : | | : : | | 486 TPPPQPLQCMEPNKEVTVSCSATGRE--KPTIQWTKTD-----GSSLPSHVSHRAG 534
                                                                                                                                                                          ILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGQYYCIASNDAG-----SARCEEQB------MEVYDLNIGGIIGGVLV 251
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A;Residues: 1-853 <LIP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLAVLALITLGICCAYRRGYFINNKQDGB 280
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Matches 60; Conserva
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OM protein - protein search, using sw model

June 15, 2004, 10:51:49; Search time 10 Seconds (without alignments) 1614.175 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-524-531C-15 1637 1 MALRRPPRLAICARLPDFFL..........VNYIRTDBEGDFRHKSSFVI 310

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_42:\* Database :

	Description	P57087 homo sapien	O88792 mus musculu	Q9y624 homo sapien	Q9xt56 bos taurus	Q99795 homo sapien	P16170 xenopus lae	.,		_	_		O15394 homo sapien	P13596 rattus norv			Q05793 mus musculu	Q91048 gallus gall	٠.		P31836 bos taurus	рошо	рошо	рошо	pomod	-			P35331 gallus gall		_	Q26474 schistocerc	homo	P10586 homo sapien
SUMMARIES	ID	JAM2 HUMAN	JAMI_MOUSE	JAM1 HUMAN	JAM1_BOVIN	A33 HUMAN	NCAI XENLA	NCA2 XENLA	AMAL_DROMB	NCA2 MOUSE	NCA1_MOUSE	NEO1_RAT	NCM2_HUMAN	NCA1_RAT	PTPD HUMAN	NCM2_MOUSE	PGBM_MOUSE	PTK7_CHICK	NCA1_CHICK	NEO1_MOUSE	NCA1_BOVIN	NTRI_HUMAN	NCA2_HUMAN	NCA1_HUMAN	CXAR_HUMAN	UN89_CAREL	CEPU_CHICK	NTRI_MOUSE	NRCA_CHICK	NTRI_RAT	NEO1_HUMAN	LACH SCHAM	CEAS_HUMAN	PTPF_HUMAN
	DB	-	Н	-	Н	-	н	Н	Н	-	-	н	н	-	-	Н	Н	-	-	-	-	<del>, -</del>	-	-	м	-4			-	-	-4	-	-	7
	Query Match Length	298	300	299	298	319	1088	1092	333	725	1115	1377	837	828	1912	837	3707	1051	1001	1493	853	344	761	848	365	6632	353	344	1284	344	1461	349	702	1897
d	Query Match	29.8	27.9	25.9	25.0	14.0	11.4	10.8	ö	٥.	10.5	10.4	10.4	10.4	10.4	10.3	10.0	•	•	•	9.9	g.	•	•	7.6		7.6			٠	•	9.3		9.0
	Score	488	457.5	424	408.5	228.5	186	177	174	171.5	171.5	171	170	169.5	169.5	169	164.5	163.5	163	163	161.5	161	160.5	160.5	159.5	159.5	159	156	155.5	155	153.5	151.5	150.5	147.5
	Result No.		7	m	₹	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q62813 rattus norv P32736 rattus norv							
LAMP_RAT OPCM_RAT	PGBM_HUMAN LAMP_CHICK	CEA1 MOUSE	CD22_HUMAN	CAME FUGRU	MU18 HUMAN	CXAR MOUSE	OPCM_BOVIN
			-	Η,		н	-
338	4391 338	521 338	847	1277	1443	365	345
89 89 6. 6.	8 8 6 6	6.8	8.8	8.6	B B	8.7	9.6
146.5	145.5 145	145	144	143.5	143.5	142	141
34	36	80 60 60 60	40	41	4 4 2 6	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 QEMBUYDINIGGIIGGULVULAVLALITIGICCAYRRGYFINNKQDGESYKNPGKPDGVN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
FUNCTION: MAY PLAY A ROLB IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MALRRPPRIRICARLPDFPLLLLFRGCLIG----AVNLKSSNRTPVVQ--EFESVELSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARRSRHRL------LILLLRYLVVALGYHKAYGRSAPKDQQVVTAVEYQEAILAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 IITDSQTSDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRNDSALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 WFYDGIRLLENPRLGSQSTNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Pred. No. 4.5e-33;
60, Mismatches 115; Indels 28; Gaps
                                                                                                                 SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
DATABASE: NAME=PROW, NOTE=PROW 2:1-3 (2001);
WWW-nhttp://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                 SUBCELLULAR LOCATION: Type I membrane protein (Potential). TISSUB SPECIFICITY: PROWINENTLY EXPRESSED ON HIGH BNDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE RNDOTHELIA OF OTHER VESSELS LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUNCTIONAL ADHESION MOLECULE 2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASHIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.8%; Score 488; DB 1; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:14686; JAM2.
MIM; 606870; --
GO; GO:0005887; C:integral to plasma membr
GO; GO:001337; P:cell-cell adhesion; NAS.
InterPro; IPR003198; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                        EMBL; AP255910; AAF81223.1; -. EMBL; AY016009; AAG49022.1; -. EMBL; BC017779; AAH17779.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIKE; 2.
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Best Local Similarity 36.2%;
Matches 115; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
238
259
259
127
238
238
214
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PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin
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DOMAIN
TRANSMEM
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293 YIRTDEEGDFRHKSSFVI 310

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MEDLINE=21391702; PubMed=11500366;

KREATURE=21391702; PubMed=11500366;

KREATURE=21391702; PubMed=11500366;

KREATURE=21391702; PubMed=11500366;

KREATURE=21391702; PubMed=11500366;

KA WINKler F.K., Hennig M.,

MINKLER F.K., Hennig M.,

"X-ray structure of junctional adhesion molecule: structural basis for normalian adhesion via a novel dimerization motif.";

EMBO J. 20:4391-4398(2001).

-I-FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.

Involved in platelet activation.

SERONIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98327120; PubMed=9660867;
Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
Simmons D., Dejana E.;
"Junctional adhesion molecule, a novel member of the immunoglobulin
superfamily that distributes at intercellular junctions and modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interaction.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21340266; PubMed=11447115;
Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
Meyer zu Brickwedde M.-K., Ohno S., Veetweber D.;
"The cell polarity protein ASIP/PAR-3 directly associates with
junctional adhesion molecule (JAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelial and endothelial cells.
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Localized at tight junctions of both
                                                                                                                                                                                                                              Junctional adhesion molecule 1 precursor (JAM) Filk OR JAM1 OR JCAM1 OR JCAM. Mus musculus (Mouse).
                                                                                                                                                                                      (Rel. 40, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                             300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monocyte transmigration.";
J. Cell Biol. 142:117-127(1998).
281 XATTMSENDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U89915; AAC32982.1; -.
                                                                                                                             STANDARD;
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MGD; MGI:1321398; Fllr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH PARD3
                                                                                                                                                                       (Rel. 40,
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                                             16-0CT-2001
                                                                                                                                                                                                            10-OCT-2003
                                                                                                                             MOUSE
                                                                                                                               JAM1 MC
088792;
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us-09-524-531c-15.rsp

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novel
   7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRPRNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPHINSETGTLVPTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLFLFTSMILGSLVQGKGSVYTAQSDVQVPRNESIKLTC--TYSGFSSPRVEWKPVQGST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVLALITIGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 LILIGILIPGVWPAYSRGYPETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSFLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LLLLFRGCLIGAV-----NLKSSNRTPVVQBFBSVELSCIITDSQTSDPRIEWKKIQDEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99323940; PubMed=10395639; Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K., Iwanatsu A., Kita T.; "Combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells."; Immunol. 163:553-557(1999).
GO; GO:0005515; P:protein binding; IPI.
InterPro; IPR00110; Ig-like.
InterPro; IPR001506; Ig_v.
PEam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PR0STR; PSS0835; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                              212 POTENTIAL.
42 N-LINKED (GLCNAC. . .) (FOTENTIAL)
185 N-LINKED (GLCNAC. . .) (POTENTIAL)
32368 MW, 331F3E48PF3E97EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.
Kornecki E.;
"Molecular cloning and sequencing of the cDNA of F11 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                     ; Score 457.5; DB 1; Length 300;
; Pred. No. 1.5e-30;
56; Mismatches 121; Indels 15.
                                                                                                                                                                   ADHESION MOLECULE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM) (Platelet adhenolecule 1) (PAM-1) (Platelet FI1 receptor) (UNQ264/PRO301)
FIIR OR JAMI OR JCAM.
                                                                                                                                                                 JUNCTIONAL ADHESION MOLEC
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
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IG-LIKE V-TYPE 2.
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185
300 AA;
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260
28
134
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Q9Y624;
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TRANSMEM
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REC MEDLINE-22386257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altasener R.D., Colling P.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altasener R.D., Colling P.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altasener R.D., Colling P.S., Wagner L., Sheafer C.F., Bhat N.K.,

RA Altasener R.D., Colling P.S., Wagner L., Sheafer C.F., Bhat N.K.,

B. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleron M., Soares W.B., Bonaldo M.F., Carswant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyvki S., Carniori P., Frange C.C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Rahes S.W., McEwan P.J., McKernan K.J., Malek J.A., Ghabs R.A.,

Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Nillalon D.K., Muzny D.M., Green E.D., Dickson M.C.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

Ruterfield Y.S.N., Krzywinski M.I., Skalsku U., Smallus D.E.,

Rocentric A. Schein J.B., Jones S.J.M., Marra M.A.;

Ruterfield X.S.N., Krzywinski M.I., Skalsku U., Smallus D.E.,

Rocentric A. Schein J.B., Jones S.J.M., Marra M.A.;

Ruterfield Acad. Sci. U.S.A. 99:16899-1690312002).

C. FURKTION: Seems to plays a role in epithelial right junction assembly (By similarity). Plays a role in regulating monocyte transmigration of the PRRD-PRAPP certified PARD3 with JAM1, thereby preventing regulating monocyte transmigration involved in platelet activation:

C. FURKLULAR LOCATION: Page I membrane protein (Potential).

Interaction of Page I membrane protein of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dowd P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22887296; PubMed=12975309; MEDLINE-22887296; PubMed=12975309; Clark H.P., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chan J., Chai C., Crowley C., Currell B., Deuel B., Dowd P. Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Sewis L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                        SEGUENCE FROM N.A.

Naik U.P., Naik M.U., DeLeon P., Spychala J.;

Cloning and characterization of PAM-1, a novel platelet adhesion molecule involved in platelet activation.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt K., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
member from human platelets.";
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epithelial and endothelial cells.
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Genome Res. 13:2265-2270(2003).
superfamily
                                                    Submitted (NOV-1999)
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ij
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10-0CT-2003 (Rel. 40, Last sequence update)
Junctional adhesion molecule 1 precursor (JAM).
PIR OR JAMI.
         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                               Bos taurus (Bovine).
                                                                                                          NCBI_TaxID=9913;
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BRML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                             pfam; PF00047; ig; 2. SMART; SM0046; IC7; 1. SMART; SM0046; IC7; 1. PROSITE; PS50835; IG LIKE; 2. Tight junction; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
D95DE2FEA23D2851 CRC64;
-!- SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
JUNCTIONAL ADHESION MOLECULE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.9%; Score 424; DB 1; Length 299; 32.8%; Pred. No. 8.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                        IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
POTENTIAL.
                                                                                                                                                                                                                    GO:0005911; C:intercellular junction; TAS. GO:0006954; P:inflammatory response; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                   EMBL; AF111713; AAD42050.1; -. EMBL; AF207907; AAF22829.1; -. EMBL; AF172398; AAD48877.1; -.
                                                                                                                                                    AL136649; CAB66584.1; -. AY358896; AAQ89255.1; -. BC001533; AAH01533.1; -.
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InterPro; IPR003596; Ig_v.
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Matches 101; Conservative
                                                                                                                                                                                               Genew; HGNC:14685; F11R.
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292 KQTSSFLV 299
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135
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153
185
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299 AA;
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JAM1_BOVIN
ID _JAM1_BOVIN
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298 AA.

PRT;

STANDARD;

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**Combined treatment of TMP-alpha and IFM-gamma causes redistribution and increment of TMP-alpha and IFM-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";

1. Jummanol. 163:53-557(1999).

2. Immanol. 163:53-557(1999).

2. Terruits RARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

2. SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity).

2. SUBCELLUIAR LOCATION: Type I membrane protein (Potential).

2. INSUR SPREIFICITY: Localized at tight junctions of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-2.
Ffan; PR00047; ig; 2.
SMART; SM00408; IGc2; 1.
PR0STR; PS550835; IG_LIKE; 2.
Right junction; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99223940; PubMed=10395639; Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K., Iwamatsu A., Kita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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211 POTENTIAL.
184 N-LINKED (GLCNAC. . .) (POTENTIAL)
32456 MM; 714FEIC1714769A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epithelial and endothelial cells.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily.
-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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Pred. No. 1.6e-26;
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EXTRACELLULAR (POTENTIAL)
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IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
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33.8%;
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152 2
184 1
298 AA;
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                                                                                                                               296
                                 NSSPHLNSETGTLVFTAVHKDDSGQYYCIASND-AGSARCBEQEMEVYDLNIGGIIGGVL 250
                                                                                                         VVLAVLALITIGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTD--EEGDFRHKSSF 308
GDIRGLVCYNNKITASYENRV-TFSDTGITFHSVTRKDTGMYTC-MVSDEGGNTYGEVTV 123
                                                                           BLTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The human A33 antigen is a transmembrane glycoprotein and a novel member of the immunoglobulin superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Colon carcinoma;
MBDLINE=97165045; PubMed=9012807;
MBDLINE=87165045; PubMed=9012807;
MBCLINE=17.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J., Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C., Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice B.C., Burgess A.W.;
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POST-TRANSLATIONAL MODIFICATIONS.
MEDLINES-97396159; PubMed-9245713;
Ritter G., Cohen L.S., Nice B.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Palmitoylated.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                OV-1997 (Rel. 35, Last sequence update)
AR-2004 (Rel. 43, Last annotation update)
surface A33 antigen precursor (Glycoprotein A33)
                                                                                                                                                                                                                                 319 AA.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                     (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U79725; AAC50957.1; -.
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LV 298
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84 -IQGDL-----AGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDBIVIELTV 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 LVPPSKPECGIEGETIIGNNIQLTCQSKGGSPTPQYSWKRYNILNQEQPLAQPASGQP-- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNSSFHIANSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE-EQEMEVYDLNIG---GII 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGVLVVLAVLALITIGICCAYRRGYPIN--NKQDG----ESYKNPGKPDGVNYI--RTDE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 VGVVAALIIIGIIIYCCCC---RGKDDNTEDKEDARPNRRAYEBP--PEQLRELSREREE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 IGAVNIKSSNRTPVVOBPESVELSCII-TDSQTSDPRIEWKKIQDEQTTYVP---PDNK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
R GO: GO: 0005888: C: proteoglycan integral to plasma membrane; TAS.

R GO: GO: 0004872; F: receptor activity; TAS.

R InterPro: J PR007110; Ig-like.

R InterPro: J PR007110; Ig-like.

R InterPro: J PR003596; Ig-v.

R PART: SMO0406; IGv; 1.

R PROSITE; PSC0315; IGV; 1.

R PROSITE; PSC0315; IGV; 1.

R TRANSMEM 22 219 CELL SURFACE A33 ANTIGEN.

T TRANSMEM 236 256 POTENTIAL).

T TRANSMEM 236 257 319 CYTOPLASMIC (POTENTIAL).

T DOWALN 22 134 IG-LIKE V.TYPE.
           to plasma membrane; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 228.5; DB 1; Length 319; 25.7%; Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule 1, 180 kDa isoform precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POLY-CYS.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. . . ) . N-LINKED (GLCNAC. . . ) . (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35632 MW; 9BPC7AAF45C2408B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] _
SROTENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180)
MEDLINE=90098871; PubMed=2481269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1088 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGDPRHK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 EDDYROE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                               DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Kenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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                      SEQUENCE
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Best Local S
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                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     ISOId=P16170-2; Sequence=VSP 002589;
-!- TISSUB SPECIFICITY: Expressed in neuron and in presumptive neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEURAL CELL ADHESION MOLECULE 1, 180 kDa
                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
                                                                       Nucleic Acids Res. 17:10321-10335(1989).
-!- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
Missing (in isoform N-CAM 140).
Krieg P.A., Sakaguchi D.S., Kintner C.R.;
"Primary structure and developmental expression of a large
cytoplasmic domain form of Xenopus laevis neural cell adhesion
molecule (NCAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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INTERPOS INTERPOSACIANT INTERPO
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HEPARIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPIASMIC (POTENTIAL).
G1-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
PIBRONECTIN TYPE-III 1.
PIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORM.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2; Name=N-CAM 180;
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N-LINKED
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PROBABLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1088
                                                                                                                                                                                                                                      Name=N-CAM 140;
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TRANSMEM
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VARSPLIC
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                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: || :: | | :: | | 214 RQL----RGENISC-DADGPPDPBISMLKKGEPIBDG-----BEKISF 260
                                                                                                                                                                                                                                                                      83 KIQGDLAGRABILGKTSLKIWNVTRRDSALYRCE--VVARND--RKBIDBIV-IELTVQV 137
                                                                                                                                                                                                                                                                                                                                                                                                           160 DV-----RFVVLANNYLQIRGIKKTDBGTYRCBGRILARGEINYKDIQVIVNVPPTIQA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHL 197
                                                                                                                                                                                                                               82
                                                                                                                                                                                                                               GAVNLK-----SSNRTPVVQBFBSVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVPPDN
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93273239; PubMed=7684721;
Tonissen K.F., Krieg P.A.;
"Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
laevis are expressed during development and in adult tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 127:243-247(1993).
-1- FUNCTION: This protein is a cell adhesion molecule involved in
neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=P36315-1; Sequence=Displayed;
SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                84; Indels 36;
                                                                                                 ; DB 1; Length 1088; 1.8e-07;
/FTIG=VSP_002589.
1088 AA; 117778 MW; 62738B55803F3B83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurites, etc.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comment=A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 NSBTGTLVFTAVHXDDSGQYYCIASNDAGSA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 NEDQSEMTIHHVEKDDEABYSCIANNQAGEA 291
                                                                                          ch 11.4%; Score 186; DB 1 Similarity 28.9%; Pred. No. 1.8e-61; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1092 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P56276; ITLK.
InterPro; IPR008957; FW III-like.
InterPro; IPR001961; FW III.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M76710; AAA49910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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"Complete
Submitted
       10;
                                                                                                                                                                                                                                                                                                                                                                GTVNLKIYQKLIPKYAPTPQEPTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIPKK 159
                                                                                                                                                                                                                                                                                                                                                                                        83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDBIVIELTVQVKPV 140
                                                                                                                                                                                                                                                                                                                                                                                                  160 DV-----RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---BINYKDIQVIVNVPPL 210
                                                                                                                                                                                                                                                                                                                                                                                                                          141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                211 IQARQIRVNATANMDESVVLSC-DADGPPDPRISWLKKGEPIEDG------EEKISFN 261
                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                       30 GAVNIKSSNR-----TPVVQEPESVELSCIITDSOTSDPR-IEWK-KIQDBQTTTVPFDN
                                                                        NEURAL CELL ADHESION MOLECULE 2, 180 kDa
                                                                                                                                                                                                                                                                                                                                      88; Indels 34; Gaps
                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                          17 N-LINKED (GLCNAC. .) (POTENTIAL)
43 N-LINKED (GLCNAC. .) (POTENTIAL)
72 N-LINKED (GLCNAC. .) (POTENTIAL)
118082 MW; CD236EE0EF8B7AD1 CRC64;
                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amalgam protein precursor.

AMA OR BG:DS00276.6 OR CG3198.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                     DB 1; Length 1092;
                                                                                                                 IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIRRONECTIN TYPE-III 1.
FIRRONECTIN TYPE-III 2.
HEPARIN-BINDING (POTENTIAL).
                                                                                          EXTRACELLULAR (POTENTIAL)
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SWART; SW00060; FN3; 2.
SWART; SW00408; IG-2: 4.
SWART; SW00408; IG-2: 4.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Immunoglobulin domain; Alternative splicing; Signal.
                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                    GLCNAC.
                                                                                                                                                                                                                                                                                                                     10.8%; Score 177; DB 1;
28.6%; Pred. No. 1e-06;
tive 28; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMAL_DROME STANDARD; PRT; 333 AA. P15364; 09V3A5; 01-APF-1990 (Rel. 14, Created) 10-CCT-2001 (Rel. 40, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                                                                                                                                                                             GLONAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                   N-LINKED
N-LINKED
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nes 60; Conservative
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SEQUENCE FROM N.A.
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and for commercial
        (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                      246 SAELEC-SVOGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEBDP 302
                                                                                                                                                                                                                                                                                                                                             94
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Noural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
NCAM-120).
                                                                                                                                                                                                                                                                                                                                           35 KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEI
                                                                                                                                                                                                                                                                                                                                                                                            155 MATLHCQESECHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDS
                                                                                                                                                                                                                                                                                                                            20; Gaps
                                                                                                                            SMARY, SM00408, IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                       AMALGAM PROTEIN.
REMOVED IN MATURE FORM (POTENTIAL)
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                     . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6;
MEDLINE-87246524; PubMed=3595563;
Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
                                                                                                                                                                                                                                                                                                        Length 333;
                                                                                                                                                                                                                                                                                                                            84; Indels
Usage by
                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (PC -> K (IN REF. 1). F644753DE3DB25F1 CRC64;
                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                        ch 10.6%; Score 174; DB 1; 1 Similarity 26.3%; Pred. No. 4.2e-07; 51; Conservative 39; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 AA.
modified and this statement is not removed.
                                          EMEL; AE001572; AAD19797.1; --
EMEL; AE003674; AAF54084.1; --
EMEL; AY051911; AAK93335.1; --
EMEL; AY051911; AAK93335.1; --
EMEL; AY051911; AAK93335.1; --
EMEL; AY051911; AMA:
GO; GO:0005886; C:plasma membrane; IDA.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_C2.
          ities requires a license agreement (send an email to license@isb-sib.ch)
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PROBABLE.
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                                     EMBL; M23561; AAA28367.1;
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                                                                                                                                                                                                                       1117
208
307
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                                                                                                                    Pfam; PP00047; ig;
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DISULPID
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        STRAIN=CS7BL/6; TISSUE=Brain;
MEDLINE=88251563; PubMed=2721486;
Santoni M.J., Barthela D., Vopper G., Boned A., Goridis C., Wille M.;
Santoni M.J., Barthela D., Vopper G., Boned A., Goridis C., Wille M.;
"Differential exon usage involving an unusual splicing mechanism
generates at least eight types of NCAM cDNA in mouse brain.";
EMBO J. 8:385-392(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.,
"Isolation and nuclectide sequence of mouse NCAM cDNA that codes for
a Mr 79,000 polypeptide without a membrane-spanning region.";
EMBO J. 6:907-914(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by a GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 642-725 FROM N.A.
MEDLINE=88283628; PubMed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
Bifferential splicing and alternative polyadenylation generates distinct NCAM transcripts and proteins in the mouse.";
EMBO J. 7:625-632(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
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InterProj. TRR003957; FN III-like.
InterProj. TRR003597; FN III.
InterProj. TRR003598; 19_c2.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; 19; 5.
SMART; SM00060; FN3; 2.
SWART; SM00060; FN3; 2.
SWART; SM00060; FN3; 2.
FR003TRF; PS50035; IG. IIKE; 5.
FR003TRF; PS50035; IG. IIKE; 5.
Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurites, etc.
SUBCELLULAR LOCATION: Attached to the membrane
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOFORM.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
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Name=N-CAM 140;
IsoId=P13595-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 20-700 FROM N.A.
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725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=N-CAM 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=N-CAM 120;
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116
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529-1115 FROM N.A. (ISOFORM N-CAM 140)
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[2]
SEQUENCE
260
                                                                                                                                                                                                                                                                                                             CVVIAEDGIQSEATVNVKIPQKLMPKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                                                                                                                    72 DEQTITYVPFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCE--VVARNDRKBIDBI 129
                                                                                                                                                                                                                                                                                                                                   130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                                                                                                                                          NCAL MOUSE STANDARD; PRT; 1115 AA.
P1355; 061949;
01-JAN-1990 (Rel. 13, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NGural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
NCAM1 OR NCAM.
                                                                                                                                                                                                                                                                                                                                              203 DIQVIVAVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGBFIENBEB-D
                                                                                                                                                                                                                                                                     CLIGA-----VNLKSSNR----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
a Mr 79,000 polypeptide without a membrane-spanning region.";
EMBO J. 6:907-914(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                           RERESENCE -> DECHLIFED (IN REF. 2).

V -> L (IN REF. 2).

QD -> XT (IN REF. 2).

T -> K (IN REF. 2).

T -> K (IN REF. 2).

MQPESS -> SANTEP (IN REF. 2).

MQPESS -> SANTEP (IN REF. 2).

PEL -> REP (IN REF. 2).

PEL -> REP (IN REF. 2).

H -> D (IN REF. 2 AND 3).

H -> D (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                    PRPRINSSFHINSETGTLVPTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                      43;
                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                      DB 1; Length 725;
                                      HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
PROBABLE.
PROBABLE.
                                                                                                                                                                                                                                                      84; Indels
                       FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                       GLCNAC.
C2-TYPE 3.
C2-TYPE 4.
C2-TYPE 5.
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                                                                                                                                                                                                                                                      41; Mismatches
                                                                                                                                                                                                                                     10.5%; Score 171.5; 27.3%; Pred. No. 1.8
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STRAIN=C57BL/6;
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PROBABLE.
IG-LIKE O
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                                                                                                                                                                                                                      80296
                                                                                                                                                                                                                                                      Conservative
                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                              657
725 AA;
                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                      63;
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DISULFID
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CARBOHYD
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MOUSE
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                       Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M., Goridis C., Wille W.;
"Analysis of cDNA clones that code for the transmembrane forms of the mouse neural cell adhesion molecule (NCAM) and are generated by alternative RNA splicing.";
Nucleic Acids Res. 15:8621-8641(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 20-36.
MEDLINE=66140120; PubMed=3512556;
Rougon G., Marshak D.R.;
Rougon G., Marshak D.R.;
Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules.";
J. Biol. Chem. 261:3396-3401(1986).
-!- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=89251563; PubMed=2721486; Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille Santoni M.J., arthels D., Vopper G., Boned B., Goridis mechanism "Differential exon usage involving an unusual splicing mechanism generates at least eight types of NCAM cDNA in mouse brain."; EMBO J. 8:385-392(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                    generates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barthels D., Vopper G., Wille W.;
"NCAM-180, the large isoform of the neural cell adhesion molecul
the mouse, is encoded by an alternatively spliced transcript.";
Nuclaic Acids Res. 16:4217-4225(1988).
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                                                                                                                                                                                                                                                                                                                                                             Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.; "Differential splicing and alternative polyadenylation distinct NCAM transcripts and proteins in the mouse.";
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                                                                                                                                                                                                                                                                                          SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180)
MEDLINE-86283628; PubMed-3336534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurites, etc.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
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Name=N-CAM 120;
Isold=Pl3594-1; Sequence=External;
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IsoId=P13595-1; Sequence=Displayed;
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EMBL; Y00051; -; NOT_ANNOTATED_CDS.
EMBL; X06328; CAA30641.1; -.
EMBL; X07244; CAA30173.1; -.
EMBL; X15051; CAA3150.1; -.
EMBL; X15052; CAA3151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUB=Brain;
MEDLINE=88247737; PubMed=2454455;
MEDLINE-88067687; PubMed=3684567;
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MGD; MGI:97281; Ncaml.
InterPro; IPR008957; FN_III-like.
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                                                                     MEDLINE=97015074; PubMed=8861902;
Keino-Masu K., Masu M., Hinck L., Leonardo B.D., Chan S.S.-Y.,
Keino-Masu K., Tessier-Lavigne M.;
Culotti J.G., Tessier-Lavigne M.;
"Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
Cell 87:175-185(1996).
-!- FUNCTION: May be involved as a regulatory protein in the
transition of undifferentiated proliferating cells to their
differentiated state. May also function as a cell adhesion
molecule in a broad spectrum of embryonic and adult tissues.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. DCC family.
-!- SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; 1PR003957; FN III-like.
InterPro; 1PR003961; FN III-like.
InterPro; 1PR003961; FN III.
InterPro; 1PR003961; FN III.
InterPro; 1PR003598; Ig_c2.
Pfam; PR00041; f3; 6.
Pfam; PR00047; ig; 4.
PRINTS; PR00060; FN3; 6.
SWART; SW0060; FN3; 6.
SWART; SW00609; IG_2; 3.
FNOSTTS; PSS0915; IG_LIKE; 4.
Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1377;
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EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
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PIBRONECTIN TYPE-III 2
PIBRONECTIN TYPE-III 4
PIBRONECTIN TYPE-III 4
PIBRONECTIN TYPE-III 5
POLY VAL.
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HSSP; P56276; ITLK.
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                                        SEQUENCE FROM N.A.
    WCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 CLIGA------VNLKSSNR-----TPVVQEFBSVELSCIITDSQTS-DPRIEWKKIQ 71
InterPro; IPR003961; FN_III.
InterPro; IPR00310; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00060; FN3; 2.
SMART; SM00060; IGc2; 5..
Cell adhesion, Glycoprotein; Transmembrane; Repeat;
Immunoglobulin, domain; Alternative splicing; Signal; Heparin-binding.
                                                                                                                                                                                                                  NEURAL CELL ADHESION MOLECULE 1, 180 kDa
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Best Local Similarity 27.3%; Pred. No. 3e-06;
Matches 63; Conservative 41; Mismatches 64; Indels 43; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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D (GLCNAC. . .) (POTENTIAL)
(in isoform N-CAM 140).
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIRENDECTIN TYPE-III 1.
FIRENDECTIN TYPE-III 1.
HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
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                                        106
                                                                                               107 RRDSALYRCEVVARNDRKEIDBIVIBLTVQVKPVTPVCRVPKAVPVGKMATLHCQBS--- 163
                                                                                                               376
                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.

MEDLINE=22660472; PubMed=12754519;
Zhang H., Li X.-J., Martin D.B., Aebersold R.;
Identification and quantification of N-linked glycoproteins using hydraxide chemistry, stable isotope labeling and mass spectrometry.";
Nat. Biotechnol. 21:660-666(2003).
-! FUNCTION: May play important roles in selective fasciculation and zone-to-zone projection of the primary olfactory axons.
-! SUBCELLUAR LOCATION: Type I membrane protein.
-! TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
                                        47 ESVELSCIITDSQTSDPRIEWKKIQDBQTTYVPFDNKIQGDLAGRABILGKTSLKIWNVT
                                                          ----EGHPRPHYSWYRN-DVPLPTDSRANPRFRNSSPHLNSETGTLVFTAVHKDDSGQ
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINB-97369930; PubMed-9226371; Paoloni-Giacobino A., Chen H., Antonarakis S.E.; Paoloni-Giacobino A., Chen H., Antonarakis S.E.; "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in
                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                e9; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 2 precursor (N-CAM 2)
31.5%; Pred. No. 4.2e-06;
tive 20; Mismatches 69
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              62; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
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Genomics 43:43-51(1997).
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 Best Local Similarity
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01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
(NCAM-140).
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 KIWNVTRRDSALYRCE--VVARNDRKBIDBIVIBLTVQVKPVTPVCRVPKAVPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AVHKDDSGQYYCIASNDAGSARCEEQEMBVYDLNIGGIIGGVLVVLAVLALITLGICCAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 NIINSDGGPYVCRATNKAG-----EDEKQAP------LQVFVQPHIIQLKNETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 RRGYPINNKQDGESYKNPGKP-----DGVNYIRTDBEGDFR-----HKSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGO-VTLVCDAE----GRPIPEITWKRAVDGFTFTEGDKSPDGRIEVKGQHGSS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . (POTENTIAL)
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                                                                                                                                                                   NBURAL CBLL ADHRSION MOLECULE 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 170; DB 1; Length 83 24.3%; Pred. No. 2.8e-06; tive 32; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C3D034106C5741C1 CRC64;
                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                    Glycoprotein; Repeat;
                                                                                                                                                                                                                                 IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PP00041; fn3; 2.
Pfam; PP00047; ig; 5.
SWART; SW0060; FN3; 2.
SWART; SW0060; FN3; 2.
SWART; SW0060; FN3; 2.
CGLI adhesion; Transmembrane; Glimmunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92932
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TRANSMEM
DOMAIN
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Matches
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00060; FN3; 2.
SWART; SM00408; IGC2; 5.
PROSITE; PSS0835; IG_LIKE; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat;
Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURAL CELL ADHESION MOLECULE 1, 140 kDa
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                    MEDIANE 90166485; PubMed=2483093; Small S.J., Haines S.L., Akeson R.A.; Small S.J., Haines S.L., Akeson R.A.; Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is developmentally regulated through alternative splicing."; Neuron 1:1007-1017(1988).
-!- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                 Small S.J., Shull G.B., Santoni M.-J., Akeson R.; "Identification of a cDNA clone that contains the complete coding sequence for a 140-kD rat NCAM polypeptide."; J. Cell Biol. 105:2335-2345(1987).
                                                                                                                                                                                                                                                                                       Isold=P13596-1; Sequence=Displayed; SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).

IG-LIKB C2-TYPB 1.

IG-LIKB C2-TYPB 2.

IG-LIKB C2-TYPB 3.

IG-LIKB C2-TYPB 4.

IG-LIKB C2-TYPB 5.

FIRBONECTIN TYPR-III 1.

FIRBONECTIN TYPR-III 2.

HEPARIN-BINDING (POTENTIAL).

HEPARIN-BINDING (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                    Comment=A number of isoforms are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M32611; AAA41679.1; ...
PIR; S00846; IJRTNC.
PDB; LRP; 27-0CT-00.
InterPro; IPR003951; FW III-like.
InterPro; IPR003961; FW III.
InterPro; IPR003961; FW III.
InterPro; IPR003961; FW III.
FRam; PP00041; fil3; 2.
Pfam; PP00041; fil3; 2.
                                           TISSUE=Brain;
MEDLINE=88059265; PubMed=3680385;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X06564; CAA29809.1; -.
                                                                                                                           SEQUENCE OF 355-364 FROM N.A.
                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                      neurites, etc.
Mammalia; Eutheri
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure
SIGNAL
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TRANSMEM
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DISULPID
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96 CVVTAEDGTQSEATVNVKIPQKLMPKNAPTPQBFKEGEDAVIVCDVVSSLPPTIIWK--- 152
                                                                                                                                                                                                                                                                                                                 27 CLIGA-----VNLKSSNR----TPVVQRFESVELSCIITDSQTS-DPRIEWKKIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.; "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Byidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 DEOTIYVPFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCE--VVARNDRKBIDBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 VIELTVOVKPVTPVCR--VPKAVPVGKMATLHCORSEGHPRPHYSWYRNDVPLPTDSRAN
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphatases.";
EMBO J. 9:3241-3252(1990).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2; Synonyme=Kidney;
IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
Name=5; Synonyme=Petal brain,
IsoId=P23468-3; Sequence=VSP 005150;
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Placenta;
MEDLINE-91006018; PubMed-2170109;
Krueger N.X., Streuli M., Saito H.;
"Structural diversity and evolution of human receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
20-20-in-tyrosine phosphatase delta precursor (RC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EK-----HIPSDDSSELTIRNVDKNDEABYVCIAENKAG-----EQDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Howo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 PRFRNSSFHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                       ; Score 169.5; DB 1; Length 858; Pred. No. 3.2e-06; 42; Mismatches 84; Indels 45
  N-LINKED (GLCNAC...) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178
MEDLINE-95204468; PubMed=7896816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P23468-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 270:6722-6728(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE OF 390-1912 FROM N.A.
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                                                                                                                                                                                                               10.4%;
                                                                                                                                                                                                                                        26.3%;
                                                                                                                                                            94658
                                                                                                                                                                                                                                                             61; Conservative
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        222
316
348
434
460
489
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                                                                                                                                                            858 AA;
                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996
10-0CT-2003
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CARBOHYD
CARBOHYD
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SEQUENCE
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SEQUENCE
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  VARSPLIC
                       VARSPLIC
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
GO; GO:0005470; F:transmembrane receptor protein tyrosine pho. .; TAS.
GO; GO:000185; F:transmembrane receptor protein tyrosine pho. .; TAS.
InterPro; IPR008957; FW III-like.
InterPro; IPR008957; FW III-like.
InterPro; IPR008361; FW III.
InterPro; IPR008362; FM III.
InterPro; IPR008389; Ig c2.
InterPro; IPR008389; Ig c2.
InterPro; IPR008389; Ig Pp.
                                                                                                                                                                                                                                                                                                                                                           Pfem; PP00102; Y_phosphatase; 2.

RR PRINTS; PR00014; PNTYPEIII.

RR SMART; SM00060; FN3; 8.

RMART; SM00040; PT05; 2.

RMART; SM00194; PTPC; 2.

RMART; SM00194; PTPC; 2.

RR PROSITE; PS00383; TYR PHOSPHATASE 1; 2.

RR PROSITE; PS0056; TYR PHOSPHATASE 2; 2.

R PROSITE; PS0055; TYR PHOSPHATASE 2; 2.

R PROSITE; PS0056; TYR PHOSPHATASE 2; 2.

R SIGNAL 1.

SIGNAL 1.
PROM THE TRANSMEMBRANB SEGMENT.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 8 fibronectin type III domains.
SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 7.
FROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHOCYSTRINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHOCYSTRINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
N-LINKED
                                                                                                                                               EMBL; L38929; AAC41749.1; -...
EMBL; X54133; CAA38068.1; -...
PIR, A56178; A56178.
HSSP; P18052; 1YFO.
Genew; HGXC:9668; PTPRD.
MIM; 601598; -...
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1137
1618
1912
1553
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                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 3
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TRANSMEM
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CARBOHYD
CARBOHYD
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DOMAIN
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13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO SVLRIQPLR----TPRDEAIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 RIPVVQEPESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVPPDNKIQGDLAGRA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
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NOM12 MOUSE
NOM2 MOUSE
STANDAM...
035136; 035962;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 GKM------ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSPHLNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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226 229 Missing (in isoform 2).

/PTIGaVSP 005148.

775 783 Missing (in isoform 2).

/PTIGaVSP 005149.

609 1137 Missing (in isoform 3).

/FTIGAVSP 005150.

1178 1178 R->A: 2.5-POLD REDUCTION IN CLEAVAGE.

1912 AA; 214759 MW; 3AB8CECD32182E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRANTH-BALBAC, TISSUB-Olfactory neuroepithelium;
MEDILINE-97368238; Pubwed-9521781;
Voshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
Kagamiyama H., Wori K.;
"OCAN: A new member of the neural cell adhesion molecule family
related to zone-to-zone projection of olfactory and vomeronasal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.4%; Score 169.5; DB 1; Length 1912;
Best Local Similarity 28.6%; Pred. No. 8.5e-06;
Matches 65; Conservative 35; Mismatches 76; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 T-----GTLVFTAVHXDDSGQYYCIASNDAGSARCEEQEMBVYDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | : | : | : | 1.1 | : | 1.2 SIGGTPIRGALQIEQSESDQGKYECVATNSAGTRYSAPANLYVREL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bvent=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.3%; Score 169; DB 1; Length 837;
Best Local Similarity 29.3%; Pred. No. 3.4e-06;
Matches 58; Conservative 25; Mismatches 79; Indels 36; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 QEF---ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 KIWNVTRRDSALYRCE--VVARNDRKEID--EIVIELTVQVKPVTPVCRVPKAVPVGKMA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 TLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSFHLMSETGTLVFTAVHKDDSGQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLFNGIGIGALIGIGVAALLILUVTDVSCPFIRQCGLLMC
TTRRNCKTSKGSGSGKSEREEREATIKOSTSTFJIVENRTE
DERTTHHEDGSPVNRENETPELTBERKL,PLKEENGTSVLNA
ETIBIKVSNDIIQSKEDDIKA -> NCCRANKGENGGSVLNA
LIANGFPFTUTMSLESCLF (in isoform short).
FTIG=VSP 002590.
70473B053A2D65A5 CRC64;
                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
vomeronasal neurons in a zone-specific manner. SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . . .) (POTENTIAL) . . . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
PIBROMECTIN TYPE-III 1.
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EMBL; AP016619; AAC53375.1;
MGD; MGI:97282; Ncam2.
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6937
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293
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Db 229 TLTCKAS-GSPDPTISWFRNGKLIE------ENEKYILKGSNTELTVRNIINKDGGS 278
Cy 217 YYCIASNDAGSARCEEQE 234
Db 279 YVCKATNKAG----EDQK 292
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Search completed: June 15, 2004, 11:03:40 Job time : 11 8ec8

4

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June 15, 2004, 10:58:19; Search time 36 Seconds (without alignments) 2716.962 Million cell updates/sec
                                                                                                                                                                1 MALRRPPRIRICARLPDFFL......VNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                               1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      protein search, using sw model
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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sp_bacteriap:*
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Maximum |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:\*

SUMMARIES

Description	ношо	OHOC	рошо	Q9d8b7 mus musculu	Q9epk4 mus musculu	Q9d1m9 mus musculu	Q9ji59 mus musculu	Qec5k9 mus musculu	Q8ce95 mus musculu	Q9jhy1 rattus norv	Q7zwt0 xenopus lae	Q8vc39 mus musculu	Q7syq7 xenopus lae	Q9y5b2 homo sapien	Q9jkd5 rattus norv	Q8bt59 mus musculu
ΩI	Q9BX67	Q8WHL8	Q96PL1	Q9D8B7	Q9EPK4	Q9D1M9	Q9JI59	Q8C5K9	Q8CB95	Q9JHY1	Q7 ZWTO	Q8VC39	Q7SYQ7	Q9Y5B2	Q9JKD5	QBBT59
BB	4	4	4	11	11	11	11	11	11	11	13	11	13	4	11	11
* Query Match Length DB	310	355	309	310	310	310	298	298	298	300	289	300	300	259	173	64
& Query Match	100.0	100.0	99.5	87.0	86.9	86.2	29.7	29.7	29.5	28.3	28.1	27.9	26.9	20.5	19.9	17.8
Score	1637	1637	1628	1425	1423	1411	486.5	486.5	483.5	463.5	460	457.5	440.5	336	326	291
Result No.	-	8	٣	4	S	9	7	80	6	10	11	12	13	14	15	16

Q9cva4 mus musculu		Q96iq7 homo sapien		OMO	Q9z109 mus musculu	Q922d5 mus musculu	Q9d2j4 mus musculu	Q9jkas musculu	Q9d0t4 mus musculu	Q9pwr4 gallus gall	Q9ygh1 gallus gall	Q91665 xenopus lae	Q90y50 brachydanio	Q9ygv5 gallus gall	Q86xk7 homo sapien	Q9h6b4 homo sapien	Q90ym0 brachydanio	Q90490 brachydanio	Q8ji27 brachydanio	Q801m2 brachydanio	Q8ay67 brachydanio	Q7z2q1 homo sapien	Q90yml brachydanio	073633 xenopus lae	Q8k1g0 rattus norv	Q9da22 mus musculu	-	Q64487 mus musculu
09CVA4	091664	096107	Q9NX42	095791	601260	Q922D5	Q9D2J4	Q9JKA5	Q9D0T4	Q9PWR4	Q9YGH1	091665	Q90Y50	Q9YGV5	Q86XK7	Q9H6B4	0MX060	090490	08J127	Q801M2	Q8AY67	Q7Z2Q1	Q90YM1	073633	Q8K1G0	09DA22	050060	064487
1	13	4	4	4	11	11	11	7	11	13	13	13	13	13	4	4	13	13	13	13	13	4	13	13	1	11	11	11
304	318	327	284	325	328	319	407	319	248	335	332	181	372	335	387	373	795	358	1409	1409	1428	259	838	725	372	300	300	1894
14.9	14.8	14.8	14.7	14.7	14.3	13.5	13.2	13.2	12.6	12.6	12.4	12.4	12.2	12.1	12.1	11.8	11.8	11.6	11.5	11.5	11.5	11.5	11.5	11.4	11.1	11.0	11.0	11.0
243.5	242	242	240.5	240.5	233.5	221.5	216	215.5	206.5	206.5	203.5	203	199.5	198.5	197.5	193.5	193.5	189.5	188.5	188.5	188.5	188	187.5	187	182.5	180.5	180.5	180.5
17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule 3 precursor (Junctional adhesion
molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
PLJ90288) (Hypothetical protein FLJ90828). [2] SEQUENCE FROM N.A.
SEQUENCE FROM N.A., Johnson-leger C., Wong C., DuPasquier L.;
Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
"Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM [3] SEQUENCE FROM N.A. Adhnson-leger C., Lamagna C., Ozaki H., Kita T.; Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.; "Junctional adhesion molecules (JAMs) and interendothelial JAM-2 OR JAM3. Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A.
Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
"Characterization of Junctional Adhesional Molecule-3 on Human
Platelets: A New Member of Immunoglobulin Superfamily."; Cunningham S.A., Arrate M.P., Tran T.M.; "Cloning of Human Junctional Adhesion Molecule 3."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. family members.";
Submitted (AUG-2001) to the RMBL/GenBank/DDBJ databases Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases 310 AA. PRT; PRELIMINARY; [1] SEQUENCE FROM N.A. TISSUE=Brain; NCBI\_TaxID=9606; unctions."; Q9BX67 RESULT 1 Q9BX67 A STATE OF S

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180

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241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 NIGGIIGGVLVVLAVLALITIGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 NDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESBGHPRPHYSMYRNDVPL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 MALRRPPRIRICARIPDFFILILIPRGCLIGAVNIKSSNRTPVVQBFESVBLSCIITDSQT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTDSRANPRFRNSSFHINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMEVYDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NDRKEIDRIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESBGHPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 PTDSRANPRFRNSSFHILNSFTGTLVFTAVHKDDSGQYYCIASNDAGSARCBEGEMBVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MALRRPPRIRICARIPDFFLLLIFRGCLIGAVNLKSSNRTPVVQBFBSVBLSCIITDSQT
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1637; DB 4; Length 355; 100.0%; Pred. No. 4.6e-153; ive 0; Mismatches 0; Indels 0
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Cardiogenesis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; AJ416101; CAC94776.1; -.
R Genew; HGNC:15532; JAM3.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR00047; Ig. 2.
R FRAM; PR000407; Ig. 2.
R SMART; SMO408; IGC2; 1.
RR SMART; ROM0408; IGC2; 1.
RR SMART; CHAIN GOMBIN.
TOTAL ADHESION MOLECULE 3.
CHAIN 76.
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TISSUE-Eye;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to 19-1ike.
InterPro; IPR003198; Ig-1ike.
R InterPro; IPR0047; ig-2.
R Pfam; PR0047; ig-2.
R Pfam; PR0047; ig-2.
R Pfam; PR0047; ig-2.
R Pfam; PR0047; ig-2.
R Pfam; PR0518; IG-2; I.
R PROSITE; PS50835; IG-LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                           CHAIN 76 355 JUNCTION ADHESION MOLECULE SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFRHKSSFVI 310
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346 DFRHKSSFVI 355
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SEQUENCE
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                                                                        P SEQUENCE FROM N.A.

18 SEQUENCE FROM N.A.

18 Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

18 Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Salto,

18 Auzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Salto,

18 Amanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

19 Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

19 Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

10 Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

21 Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.

22 Submitted (MAR-2011; -...)

23 EMBL; A2344431; CAC69455.1; -...

24 EMBL; AAV07309; BAC11195.1; -...

25 EMBL; AAV07309; BAC11195.1; -...

26 EMBL; AAV07309; BAC11195.1; -...

27 EMBL; ASV07409; BAC11195.1; -...

28 FMBL; AFONO47; ig. 2.

29 Pfam; PPO0047; ig. 2.

20 PROSITE; PSSO835; IG LIKE; 2.

20 KHYDOThetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALREPPERENCAREPPFFLELERGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTDSRANPRPRNSSFHLNSBTGTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMBVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips H.M.; "Narrowing the critical region within 11q24-qter for hypoplastic left "Narrowing the critical of a candidate gene, JAM3, expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MALRRPPRIRICARLPDPPLLLLLPRGCLIGAVNLKSSNRTPVVQBFESVBLSCIITDSQT
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                    Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIĞNAL 1 30 POTENTIAL.
SEQUENCE 310 AA; 35020 MW; CB39ADF33EA1DAB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Junction adhesion molecule 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 1637; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.8e-153;
Matches 310; Conservative 0; Mismatches 0;
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242 IGGIIGGVLVVLAVLALITLGICCAYRGYPINNKQDGESYKNPGKPDGVNYIRTDEEGD
241 IGGIIGGVLVVLAVLALITLGICCAYRGYPINNKQDGESYKNPGKPDGVNYIRTDEEGD
                                                                                                                                                                                61 DPRIEWKKIQDEQTTYVPFDNKIQGDLAGRARILGKTSLKIWNYTRRDSALYRCEVVARN
                                                                                                                                                                                                                                                                                                                 121 DRKEIDBIVIELTVAVKPUTPVCRVPKAVPVGKMATIHCQESEGHPRPHYSWYRNDVPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDSRANPRFRNSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEBQEMEVYDLN
                                                                                                                                    DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN
                                                                                                                                                                                                                                                                             DRKKIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
111000212Rik protein.
JCAM3 OR JCAM2 OR 1110002123RIK.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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86.5%;
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SMART; SM00408; IGc2; 1.
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Best Local Similarity
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MARAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,

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Saito T., Okazaki Y., Gojobori T., Bono H., Masukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Radota K., Matsuda H.A., Saito R., Nikaido I., Pesole G., Quackenbush J.,

Schinl L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G.,

Bronnetein M.J., Bult C., Pletchar C., Pujita M., Gariboldi M.,

Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Saaki H., Sato R., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wymshaw-Bronis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mymshaw-Bronis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                          SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                        1 MALSRRIALITYARLPDPFLLLLFRGCMIRAVNLKSSNRNPVVQBPBSVELSCIITDSQT
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                                            1 MALRRPPRIRICARIPDFFILLIPRGCLIGAVNIKSSNRTPVVQBFBSVELSCIITDSQT
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule-2, JAM-2 (1110002N23R1k protein)
JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
  23; Indels
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Curr. Top. Microbiol. Immunol. 251:91-98(2000)
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  19; Mismatches
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PubMed=11036763;
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobzi T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburrer M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburrer M., Batalov S., Casavant T., Radota K., Matsudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Pautuno M., Badarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Romstein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saaki H., Sato K., Schoembach C., Seya T., Shibata Y., Storch K.-P., Whitmawall H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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09JIS9
01-07CT-2000 (TTEMBLEL). 15, Created)
01-07CT-2000 (TTEMBLEL). 15, Last sequence update)
01-07CT-2003 (TTEMBLEL). 25, Last amnotation update)
01-07CT-2003 (TTEMBLEL). 25, Last amnotation addate)
03-07CT-2003 (TTEMBLEL). 25, Last amnotation addate)
03-07CT-2
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                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.; "Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.2%; Score 1411; DB 11; Length 310;
85.5%; Pred. No. 8.2e-131;
ive 20; Mismatches 25; Indels 0;
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BMBL; AK03326; BAB22715.1; -.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR00358; Ig_c2.

Ffam; PP00047; ig; 2.

SWART; SW00408; IGc2; 1.

FROSITE; PS50835; IG_IKE; 2.

Immunoglobulin domain.

SEQUENCE 310 AA; 34819 MW; 6692BCAD68BA4B1D CRC64;
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nes 265; Conservative
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|DPXHKIAFVI 310
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SEQUENCE FROM N.A.
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                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Mesonephros;
STRAIN=C354BL/6J; TISSUE=Mesonephros;
MEDLINE=23154668; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-leapth cDNAs.";
Nature 420:563-573 (2002)
Nature 420:563-573 (2002)
EMBL; AX013156; BAB28683.1; ---
EMBL; AX013156; BAB28683.1; ---
EMBL; AX012833; BAC220049.1; ---
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STRAIN-SC78L/6J; TUSBUE-Embryo;
MEDLINE-21085660; Pubmed-11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1110002N23Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
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                                                           Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00408; ĪGc2; 1.
PROSITIS, PS50835; IG_LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.9%; Score 1423; DB 11; Best Local Similarity 86.5%; Pred. No. 5.4e-132; Matches 268; Conservative 18; Mismatches 24;
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EMBL; BC024357; AAH24357.1; -.
EMBL; AK032833; BAC28049.1; -.
MGD; MGI:1933825; Jam3.
InterPro; IPR007110; IG-like.
InterPro; IPR004598; IG_C2.
Pfam; Pr00047; IG; 2.
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           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSRANPR---FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
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                                                                                                                                                                                            Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.; "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
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                    MEDLINE=20317114; PubMed=10779521;
Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
"Vascular Endothelial Junction-associated Molecule, a Novel Member of
the Immunoglobulin Superfamily, is Localized to Intercellular
Boundaries of Endothelial Cells.";
J. Biol. Chem. 275:19139-19145(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 ARLPDFFLLLLFRGCLIGAVNLKSSN------RTPVVQEFESVELSCIITDSQTSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ARSPOGLIMILLILHYLIVALDYHKANGFSASKDHRQEVTVIEFQRAILAC-KTPKKTTSS
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                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUR=Embryo, and Embryonic stem cells; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 298 AA; 33047 MW; 1124E0F07E6CF751 CRC64;
                                                                                                                                                                                                                                                         Curr. Top. Microbiol. Immunol. 251:91-98(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1933820; Jam2.
InterPro; IPR007110; Ig-like.
Pfam: PF00047; iq; 2.
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                                                                                                                                                        SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                              PubMed=11036763;
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124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analyais of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK078128; BAG37139.1; -.
MGD; MGI:1933820; Jam2.
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61 RLEWRKV-GQGVSLVYYQQALQGDFRDRAEMI-DFNIRIKNVTRSDAGBYRCEVSAPTEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ARLPDFFILLLFRGCLIGAVNLKSSN------RTPVVQBFESVELSCIITDSQTSDP
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                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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InterPro; IRR003599; Ig.
InterPro; IPR003596; Ig. C2.
InterPro; IPR003596; Ig. C2.
InterPro; IPR00409; Ig. 2.
SWART; SW00409; IG. 2.
SWART; SW00406; IGC; 2.
SWART; SW00406; IGV; 1.
PROSITE; PS06355; IGV; 1.
PROSITE; PS06355; IGV; 1.
SRQUENCE 298 AA; 33182 MW; 1131F0BFDB9CEB51 CRC64;
                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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298 AA
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
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QBCE95;
01-MAR-2003 (TrEMBLrel. 23, Created)
PRT;
                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Last an Junction cell adhesion molecule 2. JAM2 OR JCAM2.
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     PRELIMINARY;
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NDFKHTKSFII
                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Local Similarity
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TISSUE=Embryo;
    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 DSRANPR---FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMBVYD 239
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                                                                                                                                                                                                                                                                                     The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team, the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002). EMBL; AKO28757; BAC26102.1; -- KMED; MGI:1933820; Jam2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxIb=10116;
                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.5%; Score 483.5; DB 11; Length 298; Best Local Similarity 36.3%; Pred. No. 3.5e-39; Matches 113; Conservative 55; Mismatches 116; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00409; IG; 2.
SMART; SM00409; IG22; 2.
SMART; SM00408; IGC2; 2.
SMART; SM00406; IGV; 1.
SMART; PSS0835; IG LIKE; 2.
SEQUENCE 298 AA; 33079 MW; CB8227EC13D349A3 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule JAM.
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
JUCT-2003 (TrEMBLrel. 25, Last annotation update)
Junction cell adhesion molecule 2.
JAM2 OR JCAM2.
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                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-Skin;
MEDLINE-22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IRR003599; Ig.
InterPro; IRR007110; Ig-like.
InterPro; IRR003598; Ig.c2.
InterPro; IPR003596; Ig.v.
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288 NDFKHTKSFII 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PP00047; ig; 2.
                                                                                                musculus (Mouse)
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=10090;
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Q9JHY1
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  SO DE RESERVACIONES DE LA PRESENTACION DE LA PRESEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 TTYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 VQVKPVTPVCRVPKAVPVGKMATLHCQRSEGHPRPHYSWYRNDVPLPT-DSRANPRPRNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 SPHINSETGTIVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMBVYDLNIGGIIGGVLVV 252
                                                                                                                                                                                                                                                                                                                                                                                                      11 LLFLFTSMILGSLVQGKGSVYSPQTAVQVPENDSVKLPCIY--SGFSSPRVEWKFVQGST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 CLICAVNL---KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKI-QDEQTTYVPFDN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CCLWTVTLAAVTTPNPTIIVKEGBSAELQCSYSSDFTS-PRVEWKFWRDQETSFVFYDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 LAVLALITIGICCAYRRCYPINNKODGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LILLFRGCLIGA-VNLKSSNRTP----VVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Similar to junctional adhesion molecule 1.

Kenopus laevis (African clawed frog).
Makaryotas, Metazot, Chordata, Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                       ; Score 463.5; DB 11; Length 300;
; Pred. No. 3.3e-37;
49; Mismatches 121; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kiein S., Strauberg R.;
Submitted (FEB-2003) to the EWEL/GenBank/DDBJ databases.
R BMBL; BCO46720; AAH46720.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R Ffam; PF00047; ig; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00408; IG.2.
R SMART; SM00408; IG.2.
R PROSITE; PS50835; IG LIKE; 2.
R PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
28.1%; Score 460; DB 13; Length 26
Best Local Similarity 35.8%; Pred. No. 7e-37;
Matches 103; Conservative 57; Mismatches 108; Indels
STRAIN-Sprague Dawley;
Mashima H., Kojima I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP276998; AAF78250.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                    28.3%;
                                                                                                                                                                                                                                                                                                                        Matches 113; Conservative
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robert S.A., McEwan P.J., McKernan K.J., Malk J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rockiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
74 QTTYVFFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVARNDRKBIDBIVIBL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 LILIGILI PGVWFAYSRGYPERTKKG----TAPGKKVIYSQPSTRSBGBFKQTSSFLV 300
                                                                                   253 LAVLALITIGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LLLLPRGCLIGA---VNLKSSNRTPVVQBPRSVBLSCIITDSQTSD----PRIBWKKI-QDB
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                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22341132, PubMed-12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.9%; Score 440.5; DB 13; Length 34.7%; Pred. No. 6.2e-35; Arive 55; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054305; AAH54305.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AA; 32858 MW; 02BC49DC74B271D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                            300 AA
                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 25, Created)
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiative.";
Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                 01-OCT-2003
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Q7SYQ7;
                                                                                                                                                                                                                     RESULT 13
Q7SYQ7
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           KIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVARNDRKBIDBIVIELFVQVKPVTP 142
                                      SLTAPYKORA-IPYPQGITLKQITRKDAGEYSCEVTSTGSKTLYGBAKIQLQVIVAPSKP 135
                                                                                                                                                TLVFTAVHKDDSGQYYCIASNDAGSARCERQEMEVYDLNIGGIIGGVLVVLAVLALITLG 262
                                                                                                                                                                                                                                                    190 VLKFAAVSTSDSGEYYCEATNNQGKQASDLVRMDVQDVNVGGIVAAVVIVLLILALIGFG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTYVPFDNKI QGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 TALVCYNSQITAPYADRV-TPSSGITFSSVTRKDNGEYTC-MVSEGGGNYGEVSIHLT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LIFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEMKFVQGST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUB=Cecum,
MEDLINE=223546B3; PubMed=12466B51;
The FANTOM Consortium,
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
60,770 full-length cDNAs.";
EMBL; BC021B76; AAH21B76.1; -.
EMBL; AK033574; BAC28369.1; -.
                                                                                                                    VCRVPKAVPVGKMATT.HCQBSBGHPRPHYSWYRNDVPL.PTDSRANPRFRNSSPHI.NSETG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.9%; Score 457.5; DB 11; Length 300; 35.6%; Pred. No. 1.3e-36; Live 56; Mismatches 121; Indels 15;
                                                                                                                                                                                                                                                                                                                              263 ICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Junction cell adhesion molecule)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l protein.
300 AA; 32423 MW; 3CB561B8PF3B97BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AA
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GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEam; PF00047; 1g; 2. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; 1G_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, (TrEMBLrel. 20, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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01-MAR-2002
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Matches
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0890G3

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01-0CT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                          192 TYTIDPNTGVLKFASVGTSDSGEYYCKATNSQGEQSSAIVRMDVRDVNVGGIVAAVVIVL 251
134 TVQVKPVTPVCRVPKAVPVGKWATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNS 193
                                                                                                                           138 QVIVAPGTPVAQVPSSARTGSVAELMCVETQGFPLPTPTWYHNNSPWQAKS-----QNS 191
                                                                                                                                                                                                           194 SPHINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCBBQRMEVYDLNIGGIIGGVLVVL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Y., Nugrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M., Poly C., Parkos C.A.;
Foley C., Parkos C.A.;
Fluan junctional adhesion molecule is expressed by polarized columnar pinctional adhesion molecule is expressed by polarized columnar epithelia and regulates tight junction resealing.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, APIS4002; ADAPJ394-1;
InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                             254 AVLALITIGICCAYRRGYFINNKQDGBSYRONPGKPDGVNYIRTDBBGDFRHKSSFVI 310
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Best Local Similarity 29.6%; Pred. No. 1.1e-24;
Matches 81; Conservative 45; Mismatches 110; Indels 38; Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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SEQUENCE 259 AA; 20122 MW; PE3B521A911582D0 CRC64;
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Last annotation update)
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SMART; SM00408; IGc2; 1.
PROSITB; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TIDPKSGDLVFDPVSAFDSGBYYCRAQNGYGTAMRSRAVRMRAVBLNVGGIVAAVLVTLI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 HINSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVVLA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 VLALITIGICCAYRRGYFINNKQDGBSYKNPGKPDGVNYIRIDEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 173;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kirsch T., Wellner M., Haller H., Lippoldt A.;

Kirsch T., Wellner M., Haller H., Lippoldt A.;

"Cloning of the rat junctional adhesion molecule (JAM).";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; APZ41261; APZ41261; APZ41261; APZ41261; APZ61729.1;

InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
19.9%; Score 326; DB 11; Length 1'
Best Local Similarity 40.3%; Pred. No. 6.1e-24;
Matches 71; Conservative 28; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain.
NON TER 1
SEQÜENCE 173 AA; 18706 MW; 3EB3ECDFASAPB8B2 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 15, 2004, 11:05:06 Job time : 37 secs
                                                                                                                                                                                            NCBI_TaxID=10116;
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us-09-524-531c-15.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 15, 2004, 11:01:19; Search time 16.5 Seconds (without alignments) 969.942 Million cell updates/sec

Title: Perfect score:

US-09-524-531C-15 1637

1 MALRRPPRLRLCARLPDFFL.........VNYIRTDEEGDFRHKSSFVI 310 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

389414 segs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\*

(cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

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(cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

(cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

(cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

(cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Result No.	Score	Query Match	Length	DB	OI OI	Description
	1637	100.0	310	4	US-09-907-794A-423	Sequence 423, App
7	1637	100.0	310	4	US-09-905-125A-423	423,
m	1637	100.0	310	4	US-09-902-775A-423	423,
4	481	29.4	298	4	US-09-152-060-76	76, #
ß	461.5	28.2	312	4	US-09-254-465A-9	6
9	461.5	28.2	312	4	US-09-907-794A-64	64
7	461.5	28.2	312	4	US-09-905-125A-64	Sequence 64, Appl
œ	461.5	28.2	312	4	US-09-902-775A-64	64
σ,	457.5	27.9	300	4	US-09-254-465A-10	10,
10	424	25.9	299	ო	US-09-188-930-331	333
11	424	25.9	299	4	US-09-462-270-2	2, A
12	424	25.9	299	4	US-09-254-465A-1	ť,
13	424	25.9	299	4	US-09-312-283C-189	183
14	424	25.9	299	4	US-09-312-283C-331	Sequence 331, App
15	424	25.9	299	4	US-09-907-794A-119	119,
16	424	25.9	299	4	US-09-905-125A-119	119,
17	424	25.9	299	4	US-09-902-775A-119	119,
18	412	25.2	299	m	US-09-188-930-189	189,
19	392.5	24.0	260	4	US-09-254-465A-23	23
20	392.5	24.0	263	4	US-09-254-465A-25	25
21	288	17.6	205	4	US-09-462-270-4	4,4
22	228.5	14.0	319	Н	US-08-597-495B-22	22
23	228.5	14.0	319	m	US-09-068-051A-22	22,
24	228.5	14.0		4	US-09-336-536-67	67,
25	228.5	14.0		4	US-09-254-465A-6	6, 1
26	217.5	13.3	270	4	US-09-254-465A-24	24,
27	217.5	13.3	273	4	US-09-254-465A-26	Sequence 26, Appl

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Sequence Seq	earanhao
US-09-068-051A-32 US-09-175-928-2 US-09-336-536-28 US-09-336-536-28 US-09-905-125A-39 US-09-905-125A-39 US-09-905-175A-9 US-09-907-775A-39 US-09-907-775A-84 US-09-907-775A-84 US-09-905-125A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84 US-09-905-175A-84	US-08-928-383B-2
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215. 1797.5 1797.5 1609	160.5
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### ALIGNMENTS

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT PILING DATE: 2001-07-17
PRIOR PILING DATE: 2001-07-17
PRIOR PILING DATE: 2000-02-27
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-38
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                Pong, Sherman
Gao, Wei-Ciang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                 Sequence 422, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas, Daniel
Williams, P. Mickey
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Stewart, Timothy A.
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Pilvaroff, Ellen
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Paoni, Nicholas F.
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                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
US-09-907-794A-423
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SDPRIEWKKIQDEQTTYVFFDNKIQGDIAGRAEILGKTSLKIMNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALREPPELALCARL.PDFFLLLERGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRARILGKTSLKIMNVTREDSALYRCEVVAR
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                                                                                                                                                                                                                                                                                                                              and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                APPLICANT: Faui, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Stewart, Timethy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane ITITLE OF INVENTION: Secreted and Transmembrane ITITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-112
PRIOR PLILNG DATE: 1090-07-22
PRIOR PLLING DATE: 1090-07-26
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-26
PRIOR PLLING DATE: 1999-07-18
PRIOR PLLING DATE: 1999-07-18
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-10-20
PRIOR PLLING DATE: 1999-10-20
PRIOR PLLING DATE: 1999-11-20
PRIOR PLLING DATE: 1999-12-02
PRIOR PLLING DATE: 1999-12-03
PRIOR PLLING DATE: 2000-01-05
Grimaldi, Christopher J.
                    Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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CORGANISM: Homo Sapien
US-09-905-125A-423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                    PRIOR FILING DATE: 1999-121

PRIOR PELING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-00

PRIOR PLING DATE: 1999-12-00

PRIOR PLING DATE: 1999-12-00

PRIOR PLING DATE: 2000-01-05

NUMBER: PCT/USO9/00219

PRIOR PLING DATE: 2000-01-05

NUMBER: PCT/USO9/00219
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Patent No. 6664376
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bocstein, David
APPLICANT: Bocstein, David
APPLICANT: Bocstein, David
APPLICANT: Beron, Dan L.
APPLICANT: Firara, Napoleone
APPLICANT: Fivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Clang
APPLICANT: Gao, Wei-Clang
APPLICANT: Gao, Wei-Clang
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Best Local Similarity 100.0%;
Matches 310; Conservative 0
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
     FILING DATE: 1999-09-15
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US-09-907-794A-423
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APPLICANT:
APPLICANT:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE SPEREARES: P2003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT PILING DATE: 1998-09-12
RARLIER FILING DATE: 1998-03-12
RARLIER PILING DATE: 1998-03-12
RARLIER PILING DATE: 1997-03-14
RARLIER APPLICATION NUMBER: 60/040,762
RARLIER APPLICATION NUMBER: 60/040,70
RARLIER PILING DATE: 1997-03-14
RARLIER PILING DATE: 1997-03-14
RARLIER PILING DATE: 1997-03-05-30
RARLIER APPLICATION NUMBER: 60/048,100
RARLIER PILING DATE: 1997-05-30
         PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-10-30
PRIOR PILING DATE: 2000-01-05
SEQ ID NO 423
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R APPLICATION NUMBER: 60/048,189

R FLING DATE: 1997-05-30

R APPLICATION NUMBER: 60/057,765

R FILING DATE: 1997-09-05

R APPLICATION NUMBER: 60/048,970
APPLICATION NUMBER: PCT/US99/28565
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US-09-902-775A-423
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APPLICANT: Timothy A.
APPLICANT: Timothy A.
APPLICANT: Timothy A.
APPLICANT: Timos, Daniel
APPLICANT: Timas, Daniel
APPLICANT: Timas, Daniel
APPLICANT: Timas, Daniel
APPLICANT: William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
ITLE OF INVENTION: Acids Encoding the Same
FILE REPERRICE: 10466-14
CURRENT PELICATION NUMBER: US/09/902,775A
CURRENT PLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-8
PRIOR PLING DATE: 1999-07-8
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Baton, Dan L.
                                                                                                                                                                                                                                       301 DPRHKSSPVI 310
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GENERAL INFORMATION:
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PRIOR FILLING DATE: 199
NUMBER OF SEQ ID NOS:
SEQ ID NO 9
LENGTH: 312
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APPLICANT:
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Audrey
APPLICANT: Gurney, Audrey
APPLICANT: Gurney, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
                                                                                                                                                                                                                                                    LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 KRMQVDDIAISGIIAAVVVVALVISVCGLGVCYAQRKGYP--SKB--TSPQ---KSNSSS 280
                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (58); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-152-060-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 -KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFWIRIKNVTRSDAGKY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 298
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Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 35.89
Matches 114; Conservative
                                                                                                                                                                             ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                              NAME/KEY: SITE
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US-09-254-465A-9
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APPLICANT:
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S1 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107
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APPLICANT: Stewart, Timotby A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                         1 MALRRPPRIRICARLPDFFLLLLFRGCLIG----AVNLKSSNRTPVVQ--BPBSVELSC
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                         52; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 QEMEUYDLNIGGIIGGULVVLAVLALITLGICCAYRRGYF 272
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                                                                                                                                                                                             DB 4;
                                                                                                                                                                                             Score 461.5; DB 4
Pred. No. 8.1e-39;
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELING LING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
1998-09-17
                                                                                                                                                                                          Query Match
Best Local Similarity 37.1%;
Matches 104; Conservative 5.
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Mather, Jennie P.
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Eaton, Dan L.
                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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54 IITDSQFSDPRIEWKKIQDEQTTYVPFDNXIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
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CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US/09/145,698

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-16

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1999-09-17

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-11-20

PRIOR PRILICATION NUMBER: PCT/US99/2095

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR APPLICATION NUMBER: PCT/US99/30991

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30991

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30991

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR PILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel Applicant: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembran FITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14
                                                                                                                                              Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
       Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
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US-09-305-125A-64
Sequence 64, Application US/09905125A
; Patent No. 6664376
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Botstein, David
Desnoyers, Luc
Baton, Dan L
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Filvaroff, Ellen
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkemazi, Avi
APPLICANT: Botestein, David
APPLICANT: Bacon, Dan Li
APPLICANT: Ferrara, Mapole
APPLICANT: Ferrara, Mapole
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RCEVVARNDR-KBIDBIVIELTVOVKPVTPVCRVPKAVPVGKMATLHCQESBGHPRPHYS 172
                                                                                                        173 WYRNDVPLPTDSRANPRPRNSSFHINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
                                                                                                                                                                                             168 WFXDGIRLLENPRIGSQSTNSSYTWNTKTGTLQPNTVSKLDTGEYSCEARNSVGYRRCPG 227
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APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                            233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-02-2

PRIOR PILING DATE: 2000-02-2

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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APPLICATION DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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Patent No. 6686451
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Goddard, A.
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT:
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Pong: Sherman
APPLICANT: Pong: Sherman
APPLICANT: Pong: Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Napier, Martin I.
APPLICANT: Napier, Marty A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Wood, William I.
ITILE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
ITILE OF INVENTION: OF DISBASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REPREMENCE: 1920-03-05
FILE REPREMENCE: 1999-03-05
FRICH APPLICATION NUMBER: 02/09/254,465A
CURRENT FILING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-20
FRIOR PLILING DATE: 1999-03-05
FRIOR APPLICATION NUMBER: US 60/066,364
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-07
FRIOR FILING DATE: 1999-03-07
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-09-17
FRIOR FILING DATE: 1998-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCEVVARNDR-KEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WYRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 WFKDGIRLLENPRLGSQSTNSSYTWATKTGTLQPNTVSKLDTGEYSCEARNSVGYRRCPG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MALRRPPRIRICARLPDPPLLLLPRGCLIG----AVNLKGSNRTPVVQ--BPESVELSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.2
Best Local Similarity 37.1
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-64
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US-09-254-465A-10
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68 KKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNYTRRDSALYRCEVVARNDRKBID 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 PRPRNSSPHINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RKLLCL----PILAILLCSLALGSVTVHSSRPKVRIPENNPVKLSCAY--SGPSSPRVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 GGVLVVLAVLALITLGICCAYRRGYPINNKQDGBS----YKNPGKPDGVNYIRTDBEGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                      Sequence 2, Application US/09462270;
Sequence 2, Application US/09462270;
Ratent No. 6358707;
GENERAL INFORMATION:
APPLICANT: SMITHKHIDE Beecham Corporation
TITLE OF INVENTION: Human F11 Autigen: A Cell Surface
TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
FILE REFERENCE: GH-70150US
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/052,186
PRIOR APPLICATION NUMBER: 60/052,186
NUMBER OF SQL ID NOS: 4
SOTTWARE: PastSEQ for Windows Version 3.0
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241 AAVLVTLILLGILVPGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---
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Ashkenazi, Avi J.
Pong, Sherman
Goddard, Audrey
Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: HOMO SAPIENS
US-09-462-270-2
                                                                    303 RHKSSFVI 310
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292 KQTSSFLV 299
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Best Local Simil
Matches 101; C
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US-09-462-270-2
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRPRNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                   SFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCBRQEMBVYDLNIGGIIGGVLVV 252
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                                                                                                                                                                            20 LLLLFRGCLIGAV-----NLKSSNRTPVVQBFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
                                                                                                                                                                                                8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFRSVELSCIITDSQTSDPRIEW 67
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                                                                                      Ouery Match 27.9%; Score 457.5; DB 4; Length 300; Best Local Similarity 35.6%; Pred. No. 2e-38; Matches 106; Conservative 56; Mismatches 121; Indels 15;
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Sequence 311, Application US/09188930A

Patent No. 6150502

GENERAL INPORMATION:
APPLICANT: Strachan, Johnes D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, James D.
APPLICANT: Strachan, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Por Their Use
TITLE REFERENCE: 11000.1011c1
CURRENT PILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.9%; Score 424; DB 3; Length 299; 32.8%; Pred. No. 5.1e-35; Live 48; Mismatches 137; Indels
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Best Local Similarity 32.84
Matches 101; Conservative
        ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-254-465A-10
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ORGANISM: Human
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US-09-188-930-331
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48; Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
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Matches 101; Conservative
     101; Conservative
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292 KQTSSFLV 299
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US-09-312-283C-331
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LRNGTH: 299
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    9 RKILCL----FILAILLCSLALGSVTVHSSEPBVRIPENNPVKLSCAY--SGFSSPRVEW 62
                                                                                                                                                                                                                                                                                                                                                                                                               8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFBSVELSCIITDSQTSDPRIEW
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 5.1e-35;
                                                                                                                                                                                                                                                                                                                                    Length 299;
                                                                                                                                                                                                                                                                                                                                    Query Match 25.9%; Score 424; DB 4; Length 29
Best Local Similarity 32.8%; Pred. No. 5.1e-35;
Matches 101; Conservative 48; Mismatches 137; Indels
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APPLICANT: Steaman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Gleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
CURRENT APPLICATION MURBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
FILE REFERENCE: P1216R1(US)
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
FRIOR APPLICATION NUMBER: PCT/US98/24855
FRIOR PILING DATE: 1998-11-20
FRIOR APPLICATION NUMBER: US 60/066,364
FRIOR APPLICATION NUMBER: US 60/078,936
FRIOR APPLICATION NUMBER: US 60/078,936
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-17
FRIOR FILING DATE: 1998-09-17
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 189
LENCTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 189, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.9%;
32.8%;
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292 KOTSSFLV 299
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-09-254-465A-1
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                                                                               8 RLRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFBSVBLSCIITDSQTSDPRIBW
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Mathew
APPLICANT: Sleeman, Mathew
APPLICANT: Sleeman, Mathew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Murison, James G.
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----ARSEGEF 291
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APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS----
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PRIOR APPLICATION NUMBER: PCT/USO/04414

PRIOR PLING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PRILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-18

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PRIOR PLING DATE: 1999-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/28313
PILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/30095
PILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US99/28564
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PILLING DATE: 1999-12-20
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                                                                                                                                             Sequence 119, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan, James
Paoni, Nicholas F.
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Mather, Jennie P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 1999-12-02
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                                                                                                                                                                                                  Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Baton, Dan L.
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292 KQTSSFLV 299
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                                 303 RHKSSFVI 310
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US-09-907-794A-119
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                                                                                                                                                                                                                                                                     Length 299;
                                                                                                                                                                                                                                                                     Query Match 25.9%; Score 424; DB 4; Length 299
Best Local Similarity 32.8%; Pred. No. 5.1e-35;
Matches 101; Conservative 48; Mismatches 137; Indels
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USOO/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 119
LENGTH: 299
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ORGANISM: Homo sapiens
US-09-907-794A-119
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POT/4899/28313

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June 15, 2004, 10:50:54; Search time 51.5 Seconds (without alignments) 1700.771 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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1637 1 MALRRPPRIRLCARLPDFFL.......VNYIRTDEEGDFRHKSSFVI 310 US-09-524-531C-15 Title: Perfect score: 1 Sequence:

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Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A Geneseq 29Jan04:\*

11. geneseqp1980s:\*

2. geneseqp1990s:\*

4. geneseqp2001s:\*

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6. geneseqp2003as:\*

7. geneseqp2003bs:\*

8. geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	r co	PRO1868,	Human	Human	Human	Human	Human	Human PRC	Secreted	Secreted	Secreted	Human	Novel	Нишап	Нишап	Human	Human	Human	Human	Human	Novel	Нишап	Novel	Human	Human	Нимал
	Description	Aay96735	Aab33457	Aab27276	Aab80272	Aam93905	Aam93323	Aau12440	Aab80383	Aab80408	Aab80409	Abg92709	Abg91361	Abb84947	Abg65297	Abg65296	Abg65298	Abg31401	Abb95553	Abu71650	Abu72377	Abu80867	Abo17884	Abu71505	Ada57610	Ada57611
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310 6 ADAS7309 310 6 ABUS11277 310 6 ABUS1138 310 6 ABUS1314 310 6 ABUG6838 310 6 ABUG6838 310 6 ABUG6407 310 6 ABUG7314 310 6 ABUG559 310 6 ABUG559 310 6 ABUG6559 310 6 ABUG6559 310 6 ABUG6559 310 6 ABUG6813 310 6 ABUG6813 310 6 ABUG6813 310 6 ABUG6813 310 6 ABUG6813 310 6 ABUG6813 310 6 ABUG6813	Human e	Abp71277 Human jun	Human E	Human	Abo01834 Novel hum		Human	Abo47422 Human sec	Human	Novel	Human	Human	Human	Abol4925 Human Bec	Human	Human	Abu81236 Human PRO	Abu69682 Novel hum	Abol4864 Human sec	Ada46057 Novel hum	
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# ALIGNMENTS

RESULT AAY967. ID A	RESULT 1 AAY96735 LD AAY96735 standard, protein,	ırd, protein, 310 AA.
<b>1</b> 22	AAY96735;	
12	26-SEP-2000 (£	(first entry)
<b>48</b>	PRO1868, an A33	an A33 antigen homologue.
<b>€ €</b> §	PRO1868; A33 antige	PRO1868; A33 antigen; secreted protein; transmembrane protein;
ξ×	מורד-זודדמוווומרר	Aconomic Processing
3 \$	HOMIC SADTEUS.	
E	Key	Location/Qualifiers
ጀ	Peptide	1, .30
E		/label= Signal_peptide
<b>.</b> [	Modified-Bire	/b31 /
C E	Modified-Bite	/HOUSE N-HYLBLOYIBLION BILE
E		/note= "Tyrosine kinase phosphorylation site"
£	Modified-site	104107
£ 8	Modified - 01+0	/note= "N-glycosylation site"
2 &	Modified-Bire	/note= "Casein kinase II phosphorylation site"
£	Modified-site	107110
E		/note= "cAMP- and cGMP-dependent protein kinase
c s	Modified of to	prospoorylation site" 102 105
i E	שמתדדבם-פדוב	/note= "N-qlycogylation gite"
£	Modified-site	215220
£		/note= "N-myristoylation site"
<b>:</b> 6	Modified-Bite	/octo- "N-myristovlation site"
: 6:	Domain	243263
E		/label= Transmembrane_domain
E	Modified-site	243248
E E	אים ישים אין דעיאו	/note= "N-myristoylation site" 244 - 249
E	מסוווים בסוו	/note= "N-myristoylation site"
E	Modified-site	262267
E	Modified aire	/note= "N-myristoylation site" 296 .299
ZE	שַּׁחַנְינִים - מִּבְּינִים שִּׁחַנְינִים	/note= "Casein kinase II phosphorylation site"

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08-MAR-1999;
10-MAR-1999;
12-MAR-1999;
12-APR-1999;
20-APR-1999;
04-MAY-1999;
02-MAY-1999;
02-MAY-1999;
02-MU-1999;
20-JUN-1999;
20-JUN-1999;
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15.58P-1999
16.0CT-1999
29.0CT-1999
29.0CT-1999
30.NOV-1999
01.DEC-1999
01.DEC-1999
02.DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
28-JUL-1999;
01-SEP-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000
                          AAB33457;
 This is PRO1868, a putative homologue of A33 antigen, a known colorectal cancer-associated marker. The invention concerns novel secreted and transmembrane proteins, designated PRO Polypeptides. The CDNA and gene sequences are useful in the recombinant production of PRO polypeptides, as a hybridization probe to screen libraries to isolate cDNAs with sequence identity to PRO polypeptides or to map the gene encoding the PRO polypeptides and analyzing genetic disorders. The CDNA/gene can also be used to produce transgenic animals useful for the development and screening of therapeutically useful reagents. They can also be used in gene therapy, e.g. to replace a defective gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMBVYDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 300
241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDPRIBWKKIQDEQTTYVPFDNKIQGDLAGRABILGKTSLKIWNYTRRDSALYRCEVVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MALERPPELERICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MALRRPPRIRICARLPDPFILLILPRGCLIGAVNIKSSNRTPVVQEFBSVELSCIITDSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                            Perrara N, Fong S, Gao W, Goddard A;
Stewart TA, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encodes a PRO polypeptide which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 310;
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100.0%; Pred. No. 7.3e-131;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 14; 154pp; English.
                                                             9805-0113145P
9805-0113511P
9905-0115558P
9905-0115731P
9905-0119731P
9905-0119371P
                          99WO-US028634
                                                    98US-0112851P
                                                                                                                                                                          99WO-US012252
                                                                                                                                                                                                                              Desnoyers L, Po
Pan J, Roy MA,
                                                                                                                                                                                                                                                                                                                                       transmembrane polypeptide.
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Best Local Similarity 100.
Matches 310; Conservative
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|DFRHXSSFVI 310
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N-PSDB; AAA51265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 310 AA;
                          01-DEC-1999;
                                                                                                                                                                                                                           Botstein D,
                                                                                                                                                                          02-JUN-1999;
22-JUN-2000
                                                                                                      12-JAN-1999
                                                                                                                    12-JAN-1999
09-FEB-1999
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                                                                                           12-JAN-1999
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Wood WI;
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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dernatological; antiarthritic; antirheumatic; immunosuppressive; dernatological; antiarthritic; antirheumatic; immunosuppressive; heemostatic; antiallergic; antiallergic; antiallergic; hepatorropic; virucide; antiallergic; antiallergic; antiallergic; antialsematic; systemic lupus erythematosus; rheumatoid arthritis; antiatiamatory myopathy; systemic sclerosis; sarcoidosis; we diapathic inflammatory myopathy; systemic sclerosis; sarcoiditis; autoimmune haemolytic anaemis; diabetes mellitus; autoimmune thrombocytopaemia; immune-mediated renal disease; autoimmune disease; hepatobiliary disease; Whipple's disease; autoimmune disease; immune-mediated skin disease; autoimmune disease; immune-mediated skin disease; allorgic disease; immune-disease; transplantation associated disease; arguet rejection; graft-versus-host-disease.
                                                                                                                                                          Human PRO1868 protein UNQ859 SBQ ID NO:193.
AAB33457 standard; protein; 310 AA.
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99US-0123957P.
99US-0123957P.
99US-0128849P.
99WS-0131445P.
99US-0131445P.
99US-0131287P.
99WG-US01252.
99WG-US01252.
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99US-0162506P
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99WO-US028313
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99WO-US028634
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06-JAN-2000; 2000WO-US000376.
11-PEB-2000; 2000WO-US003565.
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                                                                                                    29-JAN-2001 (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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(GETH ) GENENTECH INC.

RESULT 2 AAB33457

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-Doddes, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombcorytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune of immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACSB378 graft rejection and graft-versus-host-disease. AACSB379 to AACSB379 to human PRO sequences. AACSB579 to AACSB421 and AAB33414 to AAB33477 represent human PRO polymucleotide and protein sequences given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MALRRPPRIERICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
                                                                                                                         Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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 Henzel
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Gurney AL, Hebert C, He
D, Shelton DL, Smith V;
Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1637; DB 3;
100.0%; Pred. No. 7.3e-131;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human confluency regulated adhesion molecule 1 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
KP, Goddard A,
Pan J, Pennica
, Watanabe CK,
                                                                                                                                                                                                   Claim 33; Fig 88; 309pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB27276 standard; protein; 310
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Ashkenazi AJ, Baker KP,
Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                        2000-572271/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 310; Conserv
                                                                                           N-PSDB; AAC58622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 310 AA;
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AAB27276
ID AAB3
XX
AC AAB3
XX
AC AAB3
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DT 23-1
XX
DB HURK
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The present sequence is the human confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and angiogenesis, and in the modulation of wound healing
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                                                                                                                                                                                                                                                                                                                     Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
            Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; human; confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1637; DB 3;
100.0%; Pred. No. 7.3e-131;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 6; 59pp; English
                                                                                                                                                           13-MAR-2000; 2000WO-EP002219
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Best Local Similarity 100.
Matches 310; Conservative
                                                                                                                                                                                                                                                 Imhof BA, Aurrand-Lions
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                                                                                                                                                                                                                                                                              WPI; 2000-587436/55.
                                                                                                                                                                                                                                                                                           N-PSDB; AAA95306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 310 AA;
                                                                                                 W0200053749-A2.
                                                                                                                                                                                        11-MAR-1999;
                                                                       Homo sapiens
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AAB80272
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셤
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. nererocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma. rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinits pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                     antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiathmatic; antirheumatic; cancer; antiarthitc; antinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                          PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
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V, Gerber H, Gerritsen
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100.0%; Pred. No. 7.3e-131;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                99US-0143048P.
99US-0145698P.
99US-0146222P.
99WO-US020594.
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99WO-US023089
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Wood WI;
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              Human PRO1868 protein
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Filvaroff B, F
Godowski PJ, G
                                                                                                                                                                             WO200104311-A1.
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                                                                                                                                                 Homo sapiens.
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29-NOV-1999;
30-NOV-1999;
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15-SEP-1999;
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08-SEP-1999
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NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKDDGVNYIRTDREG 300
                                                                                                                            241 NIGGIIGGVLVVIAVLALITLGICCAYRRGYFINNKQDGRSYKNPGKFDGVNYIKTDBRG 300
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          61 SDPRIEMKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                     121 NDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                             PTDSRANPRPRNSSPHLNSBTGTLVPTAVHKDDSGQYYCIASNDAGSARCBEQEMBVYDL
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T, Koga
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K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                            Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                         Human polypeptide, SEQ ID NO: 4051.
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ta T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                        (first entry)
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Ferrara N; ME, Goddard A; Kljavin IJ;

Tumas D;

Hillan KJ, Stewart TA,

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Gaps

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Length 310; Indels 9

1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT

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Best Local Similarity 100. Matches 310; Conservative

Local Similarity

Query Match

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241 NIGGIIGGYLVVLAVLALITIGICCAYRGYPINNKQDGESYKNPGKPDGVNYIRTDEBG 300
241 NIGGIIGGVLVVLAVLALITIGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEBG 300
                                                                                                                                                                                                                                                           61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRARILGKTSLKIMNVTRRDSALYRCEVVAR 120
                                                                                                                                                                                                                                                                                                                  NDRKEIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                PIDSBANPRFRNSSFHLNSETGTLVFTAVHGDDSGQYYCIASNDAGSARCEBQEMBYYDL
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                                                                                                                                                   100.0%; Score 1637; DB 4; Length 310; 100.0%; Pred. No. 7.3e-131;
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99WO-US028564.
99WO-US028565.
99WO-US02625.
99WO-US030095.
99WO-US030999.
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                                                                                                                                                                Best Local Similarity 100.
Matches 310; Conservative
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02-DRC-1999;
02-DRC-1999;
02-DRC-1999;
09-DRC-1999;
16-DRC-1999;
20-DRC-1999;
30-DRC-1999;
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                                                                                                                                                   The invention relates to primers for synthesising full length CDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful
                                                                                                                                                                                                          NDRKRIDBIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Otsuki T, Koga
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                                               Length 310;
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K, Kojima S, Otsuk
                                           100.0%; Score 1637; DB 4;
100.0%; Pred. No. 7.3e-131;
iive 0; Mismatches 0;
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                           Best Local Similarity 100.
Matches 310; Conservative
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MALRR PPRLRLCARL PDFFLLLL PRGCL I GAVNLKSSNRT PVVQBFBSVBLSCI I TDSQT

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ANUL2172-AAU1246 represent novel human secretory and transmembrane PRO
CO polypeptides. The PRO polypeptides are useful to detect other PRO
CO polypeptides, to link biactive molecules to calls expressing PRO
CO polypeptides, to modulate biological activities of cells expressing PRO
CO polypeptides, and to detect the presence of mammalian lung, colon,
CO polypeptide expression in a cell sample to that in a control sample. Some
CO polypeptide expression in a cell sample to that in a control sample. Some
CO polypeptide expression in a cell sample to that in a control sample. Some
CO polypeptide expression in a cell sample to that in a control sample. Some
CO differentiation of chondrocytes, the proliferation or gene expression in
CO pericyte cells, the release of proteoglycans from cartilage, the
CO proliferation of inner ear utricular supporting cells or of T-
CO lymphocytes, the proliferation of endothelial cells or of T-
CO lymphocytes, the proliferation of endothelial cells. Some of the PRO
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CO PROMES, or the proliferation of endothelial cells. Some of the PRO
CO PROMES, or the proliferation of endothelial cells. Some of the PRO
CO PAPPEDIGES can be used to generate probes, antisense RNA/DNA,
CO PAPPEDIGES on an enimals and can be used in gene therapy
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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2000WO-US005841.
2000US-0187202P.
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2000WO-US007377.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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N-PSDB; AAS21512.
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                                                                                     06-JAN-2000; 211-FBB-2000; 218-2000; 224-FBB-2000; 24-FBB-2000; 24-FBB-2000; 24-FBB-2000; 201-MAR-2000; 20-MAR-2000; 21-MAR-2000; 21-MAR-2000; 21-MAR-2000; 22-MAR-2000; 22-MAR-2000; 22-MAY-2000; 22-MA
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61 SDPRIEMKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSLKTWNVTRDSALYRCEVVAR 120
                                                                                                     NDRKEIDBIVIELTVQVKPVTPVCRVPRAVPVGRMATLHCQESBGHPRPHYSWYRNDVPL 180
                                                                                                                     121 NDRKEIDBIVIELTVQVKPVTPVCRVPKAVFVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                   PTDSRANPRPRNSSFHLNSBTGTLVFTAVHKDDSGQYYCIASNDAGSARCBBQEMEVYDL 240
                                                                                                                                                                                   241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
                                                                                                                                                                                                                                              241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKFDGVNYIRTDEEG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.
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1 MALRRPPRIRICARLPDPFLILLFRGCLIGAVALKSSNRTPVVQBFBSVBLSCIITDSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA;
                                          61 SDPRIEWKKIODEOTTYVPPDNKIOGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR
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Komatsoulis GA;
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Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 538-539; 601pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein encoded by gene #13
                                                                                                                                                                                                                                                                                                                                                                                                         AAB80383 standard; protein; 310 AA.
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Olsen HS,
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                                                                                                                                                                                                                                                                                                                 301 DPRHKSSFVI 310
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Lafleur DW,
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Shi Y, Laf
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Sequence 310 AA;

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Ouery Match 100.0%; Score 1637; DB 4; Length 310; Best Local Similarity 100.0%; Pred. No. 7.3e-131; Matches 310; Conservative 0; Mismatches 0; Indels 0

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                                                                                                                                                                      MALRRPPRIRICARLPDFFILLIFRGCLIGAVNIKSSNRTPVVQEFESVELSCIITDSQT
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                                                    1 MALRRPPRIRICARIPDPFLLLIFRGCLIGAVNLKSSNRTPVVQEFBSVELSCIITDSQF
                                                                                                                                                         NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
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  Length 310;
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Komatsoulis GA;
                          Indels
100.0%; Score 1637; DB 4;
100.0%; Pred. No. 7.3e-131;
iive 0; Mismatches 0;
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Birse CB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein encoded by gene #38
                                                                                                                                                                                                                                                                                                                                                                                                        AABB0408 standard; protein; 310 AA
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Olsen HS,
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                             Conservative
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              al Similarity
310; Conser
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Matches 31
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241 NIGGIIGGVLVVLAVLALITIGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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                                                                                                                      SDPRIEWKKIODEOTTYVPFDNKIOGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR
                                                                                                                                                                                      PIDSRANPRERNSSFHIASETGTLVFTAVHKDDSGQYYCIASNDAGSARCEBORMEVYDL
                                                                                   1 MALRRPPRIRICARLEDFFILLTFRGCLIGAVNLKSSNRTPVVQRFSSVBLSCIITDSQT
                                                                                                                                   SDPRIEWKKIQDBQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNYTRDSALYRCEVVAR
                                                                                                                                                                       NDRKEIDBIVI BLTVQVKPVTPVCRVPKAVPVGKMATLHCQBSECHPRPHYSWYRNDVPL
                                                                     1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT
                                              Gaps
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                      Length 310;
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                      100.0%; Score 1637; DB 4;
100.0%; Pred. No. 7.3e-131;
ive 0; Mismatches 0;
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Olsen HS,
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                                   Best Local Similarity 100. Matches 310; Conservative
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Sequence 310 AA;
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liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
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                                                                                                                                                                                                                                                  PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
                                                                                                                             1 MALRRPPRIALCARLPDFFLLLLFRGCLIGAVNIKSSNRTPVVQEFESVELSCIITDSQT
                                                                                                                                                                     SDPRIBWKKI ODEOTTYVPFDNKI OGDLAGRABILGKTSLKI WNVTRRDSALYRCEVVAR
                                                                                                                  1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFBSVBLSCIITDSQT
                                                                                                Gaps
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                                                                             Length 310;
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                                                                           Score 1637; DB 4;
Pred. No. 7.3e-131;
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                                                                           Query Match 100.0%; Score 1637; Best Local Similarity 100.0%; Pred. No. 7.3 Matches 310; Conservative 0; Mismatches
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98US-011345P.
98US-011351P.
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DFRHKSSFVI 310
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                                                          Sequence 310 AA;
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10-FEB-1999;
12-FEB-1999;
                                       preparations
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22-DEC-1998;
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16-DEC-1998;
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The invention relates to an isolated polypeptide having at least 80% amino acid sequence identity to secreted and transmembrane polypeptides pro1801, PRO18197, PRO1868, PRO1814 or PRO1801, PRO18197, PRO1868, PRO1814 or PRO180197, PRO1801, PRO1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted and transmembrane polypeptides and polynucleotides useful for diagnosis and treatment of inflammatory disorders and immune-related diseases, and identifying modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W, Goddard A;
Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1637; DB 5;
100.0%; Pred. No. 7.3e-131;
ive 0; Mismatches 0;
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Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 14; 125pp; English
                                                                99WO-US028534.
99WO-US028551.
99US-0170262P.
2000WO-US003565.
2000WO-US004414.
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2000US-0187202P.
2000WO-US008439.
2000WO-US014941.
2000WO-US015264.
   99WO-US012252
99US-0162506P
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Pan J, Roy MA,
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02-JUN-1999;
29-OCT-1999;
01-DEC-1999;
02-DEC-1999;
09-DEC-1999;
11-FBB-2000;
22-MAR-2000;
30-MAR-2000;
30-MAR-2000;
30-MAR-2000;
02-JUN-2000;
02-JUN-2000;
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Wood WI;
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23-JUN-2000; 2000US-0213637P.
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241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNRODGRSYRNPGKPGVPVYIRTDEBG 300
                                                                                                                                                         Human; secreted protein; transmembrane protein; gene mapping; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new human secreted and transmembrane proteins (PRO) and nucleic acids of the invention. The polypeptides can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N, Fong S, Gao W, Goddard A;
Stewart TA, Tumas D, Watanabe CK;
                                                                                           ABG91361 standard; protein; 310 AA.
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                                                                                                                                         Novel human secreted protein #7
                                                                                                                                                                                                                                                                   9805-0113511P.
9905-0115558P.
9905-01155533P.
9905-0119731P.
9905-0119537P.
9905-0119537P.
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2000WO-US014941.
2000WO-US015264.
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2000US-0187202P.
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25-MAY-2001; 2001US-00866034
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Pan J, Roy MA,
                                                                                                                          (first entry)
                                               DPRHKSSFVI 310
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N-PSDB; ABS67460.
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22-FKB-2000;
02-MAR-2000;
03-MAR-2000;
30-MAR-2000;
30-MAY-2000;
                                                                                                                                                                                 sapiens
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02-JUN-1999;
29-OCT-1999;
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                                                                                                                          29-NOV-2002
                                                                                                                                                                  immunogenic.
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12-JAN-1999
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                                                                                                           ABG91361;
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administered therapeutically, especially by expressing encoding polymucleotides, e.g. in therapeutic compositions. They can be used to screen for PRO polymetide antagonists and agonists useful to identify drug candidates. They can also be used to produce antibodises, useful to detect PRO polymeptides (e.g. diagnostically), purify PRO polypeptides or therapeutically (e.g. as antagonists or to target and/or deliver cytocoxic agents). The polymucleotides are useful therapeutically e.g. to produce antisense sequences to inhibit polypeptide production. They can be used to produce probes and primers useful to detect or isolate sequences encoding PRO polypeptides or similar sequences e.g. variants or sequences from other species. They are also useful for gene mapping and to generate transgenic animals. ABG91155-ABG91361 represent human PRO amino acid sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDSRANPRFRISSFHLASFTGTLAFTAVHKODSGQYYCIASNDAGSARCEEGBHWYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1637; DB 5; Length 310; 100.0%; Pred. No. 7.3e-131; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 310 AA;
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1 MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFBSVELSCIITDSQT

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ABL88002 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polymuclectides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymuclectides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, traum, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, ampangina, myccardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynuclectides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping, ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber H, Gerritsen NB, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Paoni NP;
CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
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28-FEB-2001; 2001UO-USO06520
01-MAR-2001; 2001US-00802706.
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10-MAY-2001; 2001US-00854208
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01-JUN-2001; 2001WO-US017800.
                                                                                            2000MO-US023522.
2000MO-US023328.
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22-MAR-2001; 2001US-00816744
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2001US-00854280
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2000WO-US030873
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JF, Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-090516/12.
N-PSDB; ABL88202.
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           25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
18-SEP-2000;
18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
10-NOV-2000;
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Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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therapeutic procein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosting disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
                                                                                                                                                                                         241 NIGGIIGGYLVVLAVLALITIGICCAYRRGYFINNKODGESYRNPGKPDGVNYIRTDBEG 300
241 NIGGIIGGYLVVLAVLALITIGICCAYRRGYFINNKQDGESYRNPGKPDGVNYIRTDEEG 300
             61 SDPRIEWRKIQDEQTTYVFPDNKIQGDLAGRAEILGKTSLKIMNYTREDSALYRCEVVAR 120
                                                             180
                                                                              240
                                                                                                                            PTDSRANPRFRNSSFHLNSBTGTLVFTAVHKDDSGQYYCIASNDAGSARCBGEMBVYDL
                                                                                                                                               NDRKBIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; hasmacopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti:HIV; antidiabetic; hasmostatic; nootropic; neuroprotective; antipparkinsonian; antimicrobial; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human albumin fusion protein #1972.
                                                                                                                                                                                                                                                                                                                                                                            ABG65297 standard; protein; 310 AA.
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21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic, antiarthritic.
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disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haemacopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis) ABG63326-ABG65518 represent albumin fusion proteins of the invention
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albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. acquired immunodeficiency syndrome, AIDS), emodorine disorders (e.g. acquired haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, creutzfeldt-lacob disorders (e.g. Alzheimer's, and connective disorders (e.g. diabetes), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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                                                                                                                                                      The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum
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                                                       New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
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                                                                                                                 Claim 1; Page 1893-1894; 2102pp; English.
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Aay966294
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Abg71401 Aab27278 1586107 5.1.6 Compugen Ltd. Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues SUMMARIES GenCore version Copyright (c) 1993 - 2004 Post-processing: Listing first 45 summaries sw model AAB27276 AAB80272 AAM93905 AAU12440 AAB80383 AAB80408 AAB80409 ABG92709 ABB84947 ABB65297 ABG65297 ABG65296 AAB27278 AAM93323 OLIGO Gapop 60.0 , Gapext 60.0 geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1990s: \*
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	26	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; mouse; confluency regulated adhesion molecule 1; CRAM-1; JAM-2. Murine confluency regulated adhesion molecule 1. AAB27278 standard; protein; 310 AA 13-MAR-2000; 2000WO-BP002219. 99EP-00200746 Imhof BA, Aurrand-Lions M; (first entry) (RMFD-) RMF DICTAGENE SA. WPI; 2000-587436/55. N-PSDB; AAA97189. WO200053749-A2 11-MAR-1999; 23-FEB-2001 14-SEP-2000. AAB27278; Mus sp. RESULT 1 AAB27278 

Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.

Example; Fig 8; 59pp; English.

The present sequence is the murine confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (1g Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and anglogenesis, and in the modulation of wound healing

Sequence 310 AA

Human alb Human alb Human alb Human PRO

Human PRO

Human ang Human PRO Novel hum

ABB95553 ABU71650 ABU72377

Score 310; DB 3; Length 310; Pred. No. 2.4e-288; 100.0%; Query Match Best Local Similarity

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                                                                                                SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
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  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
 Conservative
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100.0%; Score 310; DB 3; Length 310;

Query Match

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                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polynucleotide sequences given in AAC74223-C74279 encode the human secreted proteins represented in AAB3917-B39226. Sequences AAB39227-B39308 are alternative proteins encoded by the genes, and also protein sequences with which they share homology. The proteins have activities
                                                                                                                      SDPRIEWKKIQDGGTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL
                                                                                                                                                                                                                                                                                            SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL
                                                                                                                                                                                                                     PIDSRANPRPQNSSFHVNSBTGTLVPNAVHKDDSGQYYCIASNDAGAARCBGQDMBVYDL
                                                                                                                                                                                                                                      PTDSRANPRPQNSSFHVNSRTGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL
                                                                                                                                                                                                                                                                              241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGRSYKSPGKHDGVNYIRTSBRG
                                                  1 MALSRRIRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPWHEFESVELSCIITHSQT
                                                                                                                                                               NDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein sequence encoded by gene 15 SRQ ID NO:134.
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                       Indels
        Pred. No. 2.4e-288;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 32; 434pp; English
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100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                         Conservative
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                                                                                                                                                                                                                                                                                                                                    DPRHKSSPVI 310
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                                                                                                                                                                                                                                                                                                                                                       DPRHKSSPVI
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        Best Local Similarity
Matches 310; Conserv
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RESULT 5
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         activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and optialmalogical. The human secreted proteins, polymucleotides, and optialmalogical. The human secreted proteins, polymucleotides, antagonists and agonists of the invention may be useful in the treatment, prevention, and/or diagnosis of various disease disorders and conditions such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid sound chealing and epithelial cell proliferation, to regenerate tissues, maintain organs before transplantation, in chemotaxis and as a food additive or preservative e.g. to increase storage capabilities. Sequences AAC74214-C7422 and AAB19178 are used during the isolation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
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                                                                                                                                                                                                                                                                                                    Gaps
on the tissues and cells in which they are expressed. Examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                          7.7%; Score 24; DB 3; Length 285; 00.0%; Pred. No. 2.3e-14;
                                                                                                                                                                                                                                                                                                    0; Indels
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Best Local Similarity 100.04; Pred. No. 2.3
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                                                                                                                                                                                                                                                                                                                               167 PRPHYSWYRNDVPLPTDSRANPRP 190
                                                                                                                                                                                                                                                                                                                                              142 PRPHYSWYRNDVPLPTDSRANPRF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #4636
                                                                                                                                                                                                                                                                                                                                                                                                                        ABG04645 standard; protein; 291 AA
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23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                   Sequence 285 AA;
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c genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunoglobulin; IGPAM-6; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 24; DB 4; Length 291; 100.0%; Pred. No. 2.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; Pred. No. 2.3 les 24; Conservative 0; Mismatches
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Yang J;
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/label= signal_peptide
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| label = Ig_domain
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98US-0113635P.
99US-0128194P.
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Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; AAA27386.
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22-DEC-1998;
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Peptide
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Matches
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2000-431586/37.
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ses 24; Conserv
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                                                                                 MO200036102-A2
                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                     12-FBB-1999;
02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                         The present sequence is the human immunoglobulin superfamily protein IGPAM-6. Its gene was isolated from a cDNA library of leg tissue. It is expressed in reproductive, nervous and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohm's disease, diabetes mallitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodiallysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory; cytostatic; recombinant production; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "cAMP- and cGMP-dependent protein kinase
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/note= "N-glycosylation site"

/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO1868; A33 antigen; secreted protein; transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 3; Length 310;
Pred. No. 2.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243. 263
/label=Transmembrane_domain
243. 248
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244. .249
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "N-myristoylation site"
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/hore= "N-glycosylation site"
215. .220
/hote= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Stoc. No. 100.0%; Pred. No. 0; Mismatches
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation site"
                                                                             Claim 1; Page 82-83; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96735 standard; protein; 310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO1868, an A33 antigen homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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AAY8

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This is PRO1868, a putative homologue of A33 antigen, a known colorectal cancer-associated marker. The invention concerns novel secreted and transmembrane proteins, designated PRO polypeptides. The cDNA and gene sequences are useful in the recombinant production of PRO polypeptides, as a hybridization probe to screen libraries to isolate cDNAs with sequence identity to PRO polypeptides or to map the gene encoding the PRO polypeptides and analyzing genetic disorders. The cDNA/gene can also be used to produce transgenic animals useful for the development and screening of therapeutically useful reagents. They can also be used in gene therapy, e.g. to replace a defective gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encodes a PRO polypeptide which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fong S, Gao W, Goddard A
A, Tumas D, Watanabe CK;
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                                                 296. .299
/note= "Casein kinase II phosphorylation site"
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/note= "N-myristoylation site" 296. .299
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98US-0113145P.
98US-0115558P.
99US-0115558P.
99US-0115558P.
99US-0115573P.
99US-0119341P.
99US-0119517P.
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idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Mhipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease. 

Homo sapiens

WO200053758-A2

14-SEP-2000

02-MAR-2000; 2000WO-US005841

99US-0123618P. 99US-0123957P. 99US-0125775P. 99US-0128849P. 99WO-US008615. 99US-0131445P. 99US-0132371P. 99US-0134287P. 28-APR-1999; 04-MAY-1999; 14-MAY-1999; 20-APR-1999

99US-0144758P. 99US-0145698P. 99US-0146222P. 99WO-US012252 99US-0141037P 02-JUN-1999; 20-JUL-1999

99WO-US020944. 99WO-US021090. 99WO-US021547. 99WO-US020111. 01-SEP-1999; 08-SEP-1999; 15-SEP-1999;

99US-0162506P. 99WO-US028214 99WO-US028313 99WO-US023089 05-0CT-1999; 29-NOV-1999; 15-SEP-1999;

99WO-US028409. 99WO-US028301. 99WO-US028634. 99WO-US028564. 99WO-US028551 30-NOV-1999; 01-DEC-1999; 02-DEC-1999; 02-DEC-1999;

99WO-US028565. 99WO-US030999 20-DEC-1999; 30-DEC-1999;

30-DBC-1999; 99WO-US031274. 05-JAN-2000; 2000WO-US000219. 06-JAN-2000; 2000WO-US000277. 06-JAN-2000; 2000WO-US000376. 18-FBB-2000; 2000WO-US004342 22-FBB-2000; 2000WO-US00414 11-FRB-2000; 2000WO-US003565 18-FRB-2000; 2000WO-US004341

(GETH ) GENENTECH INC.

Gurney AL, Hebert C, Henzel W; D, Shelton DL, Smith V; Wood WI, Yan M; Goddard A, J, Pennica Watanabe CK, Ashkenazi AJ, Baker KP, Gov Vahaknff RC. Lu Y, Pan J, Tumas D, Stewart TA,

WPI; 2000-572271/53. N-PSDB; AAC58622.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 88; 309pp; English

The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
C selected from systemic lupus erythematosus, rheumatoid arthritis,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC systemic sclerosis, idiopathic inflammatory byopathies, Sjogren's
CC systemic sclerosis, idiopathic inflammatory byopathies, Sjogren's
CC shadmin, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC crimmune-mediated skin diseases, inflammatory bowel
CC diseases of the lung, and transplantation associated diseases including
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC represent PCR primers and hybridisation probes used in the isolation of
C human PRO polynucleoide and protein sequences given in the
CC exemplification of the present invention ô or 2 (CRAM-1 or Gaps Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability. Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; human; confluency regulated adhesion molecule 1; CRAM-1; JAM-2. ö 7.7%; Score 24; DB 3; Length 310; Indels Human confluency regulated adhesion molecule 1 #2 Pred. No. 2.5e-14; 100.0%; Prec. ...ive 0; Mismatches 167 PRPHYSWYRNDVPLPTDSRANPRF 190 167 PRPHYSWYRNDVPLPTDSRANPRF 190 AAB27276 standard; protein; 310 AA 13-MAR-2000; 2000WO-EP002219. 11-MAR-1999; 99EP-00200746. Imhof BA, Aurrand-Lions M; 23-PBB-2001 (first entry) Local Similarity 100. 1es 24; Conservative (RMFD-) RMF DICTAGENE WPI; 2000-587436/55. N-PSDB; AAA95306. Sequence 310 AA; WO200053749-A2. Homo sapiens. 14-SEP-2000, AAB27276; Query Match Best Loc Matches RESULT 8888888888888888888888 ઠે 셤 

The present sequence is the human confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and anglogenesis, and in the modulation of wound healing Claim 2; Fig 6; 59pp; English.

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Local Similarity
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                                                                                                                            Sequence 310 AA;
                                                                                                       gene mapping
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                                                                                                                                               Query Match
                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                          antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                                                                                                                                                                                                                    Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                    Gaps
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E, Goddard A;
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H, Gerritsen MB, Goddaró
Hillan KJ, Kljavin IJ;
Stewart TA, Tumas D;
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                              DB 3; Length 310;
2.5e-14;
hes 0; Indels
                              7.7%; Score 24; DB 100.0%; Pred. No. 2.5
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I, Gerber H,
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P, Roy MA,
                                                                       167 PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                   167 PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                                                                                 AAB80272 standard; protein; 310 AA
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J, Grimaldi CJ, Gurr
Pan J, Paoni NF, F
M, Wood WI;
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99WO-US028565.
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99WO-US021090,
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                                                                                                                                                                                         (first entry)
                                       Local Similarity 100.
ses 24; Conservative
                                                                                                                                                                                                               Human PRO1868 protein.
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N-PSDB; AAF72433
          Sequence 310 AA;
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Filvaroff B, B
Godowski PJ, C
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29-NOV-1999;
30-NOV-1999;
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                                                                                                                                                                                                                                                                                                             Homo sapiens
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20-DEC-1999;
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02-DEC-1999;
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                               Query Match
                                                    Matches
                                                                                                                                       RESULT 9
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The present sequence is one of sixty one novel secreted and transmembrane

Claim 1; Fig 124; 393pp; English.

disease)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and their use
PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatorid arthritis, multiple sclerosis), inflammatory infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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su A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
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                                                                                                                                                                                                                                                                                                                                 7.7%; Score 24; DB 4; Length 310; 100.0%; Pred. No. 2.5e-14; ative 0; Mismatches 0; Indels
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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RESULT 11 AAM93323

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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                                                                                              Human PRO1868 polypeptide sequence.
                        AAU12440 standard; protein; 310 AA.
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99WO-US028565.
99US-0170262P.
99WO-US030095.
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2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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2000MO-US005004.
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2000WO-US006319.
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24-AUG-2000; 2000WO-US023328
08-NOV-2000; 2000WO-US030873.
10-NOV-2000; 2000WO-US030873.
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Gerritsen MB, Goddard A,
Smith V, Stewart TA, Tum
                                                                                                                (first entry)
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09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their use
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
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                                                DB 4; Le 2.5e-14;
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100.0%; Pred. No. 2.5e-14;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                         AAM93323 standard; protein; 310 AA
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                       Ouery Match
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Matches 24; Conservative
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les 24; Conserv
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Sequence 310 AA;
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Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO

Gao W;

Best Loca Matches

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polypeptides. The Properties are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the proliferation of endothelial cells or of T-lymphocytes, the proliferation of endothelial cells or of T-lymphocytes, or the proliferation of endothelial cells or of the PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The problem of encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                   AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
      detect the presence of mammalian tumors e.g. lung, cervical.
                                                                                          Claim 12; Fig 538; 813pp; English.
   polypeptides, and breast, prostate,
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ö 7.7%; Score 24; DB 4; Length 310; 0; Indels Pred. No. 2.5e-14; 100.0%; Prec. ... 167 PRPHYSWYRNDVPLPTDSRANPRF 190 167 PRPHYSWYRNDVPLPTDSRANPRF 190 24; Conservative Local Similarity Query Match Matches ઠે 유

RESULT 1: AABB0383

AAB80383 standard; protein; 310 AA

AAB80383;

(first entry) 24-APR-2001 Secreted protein encoded by gene #13

Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; 

cerebrovascular; infection; food

Homo sapiens

WO200107459-A1

01-FEB-2001.

20-JUL-2000; 2000MO-US019735.

(HUMA-) HUMAN GENOME SCI INC

23-JUL-1999; · 99US-0145220P.

PA; Moore DR, Ni J, Soppet DR Komatsoulis GA; Duan RD, Birse CE, Ebner R, Olsen HS, I, Ruben SM, Lafleur DW, Rosen CA,

WPI; 2001-123261/13.

New isolated nucleic acid encoding 29 secreted proteins, for diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism

Claim 11; Page 538-539; 601pp; English.

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invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
                       present invention relates to 29 human secreted proteins. The
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Sequence 310 AA;

Gape ö Length 310; Indele DB 4; Ler . 2.5e-14; .ches 0; 100.0%; Pred. ... 7.7%; Score 24; Conservative Local Similarity les 24; Conserv Query Match Best Loc Matches

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167 PRPHYSWYRNDVPLPTDSRANPRF 190 167 PRPHYSWYRNDVPLPTDSRANPRF 190 ሯ

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RESULT 14 AAB80408

AAB80408 standard; protein; 310

AAB80408;

(first entry) 24-APR-2001

Secreted protein encoded by gene #38

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Gaps

Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food. 

Homo sapiens

WO200107459-A1.

01-FEB-2001

20-JUL-2000; 2000WO-US019735.

99US-0145220P. 23-JUL-1999;

(HUMA-) HUMAN GENOME SCI INC.

Moore PA; Ni J, Soppet DR, Komatsoulis GA; Duan RD, Birse CB, Ebner R, Olsen HS, Ruben SM, Lafleur DW, Rosen CA, Shi Y,

WPI; 2001-123261/13

New isolated nucleic acid encoding 29 secreted proteins, for diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism infections.

Claim 11; Page 557-558; 601pp; English.

The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardioa rarrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food preparations

Sequence 310 AA;

Gaps ő 7.7%; Score 24; DB 4; Length 310; 100.0%; Pred. No. 2.5e-14; 0; Indels Local Similarity 100.0%; Pred. No. 2.5 tes 24; Conservative 0; Mismatches Query Match Best Loca Matches

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The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food preparations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding 29 secreted proteins, for diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism
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Komatsoulis GA;
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PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                                                                                                                    Secreted protein encoded by gene #39.
                                                                                                AAB80409 standard; protein; 310 AA.
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Shi Y, Lafleur DW, Olsen HS,
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Gaps ö 7.7%; Score 24; DB 4; Length 310; 100.0%; Pred. No. 2.5e-14; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
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Search completed: June 15, 2004, 11:09:56 Job time : 51 secs

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APPLICANT: Paoni, James F.
APPLICANT: Paoni, James F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart. Timothy A.
APPLICANT: Trunchy A.
APPLICANT: Trunchy A.
APPLICANT: Twas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT PILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR PILING DATE: 1999-07-26
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: PCT/US99/20594
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US-09-907-794A-423
'S Sequence 423, Application US/09907794A
'Petent No. 6635468
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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APPLICANT: Genentech, Inc.
APPLICANT: Bakkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary B.
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Mather, Jennie P.
Pan, James
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30177, A
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25, Appl
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                                                                                                                   June 15, 2004, 11:08:05; Search time 16.5 Seconds (without alignments) 969.942 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-125A-423

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US-08-482-110C-65

US-08-484-211C-65

US-08-906-616-65

US-08-906-616-65

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US-08-906-616-65

US-08-912-411-65

US-09-012-411-65

US-09-012-62-65

US-09-012-62-65

US-09-012-62-65

US-09-012-62-65

US-09-012-62-127

US-09-134-01C-3209

US-08-906-616-127

US-08-906-16-127

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US-08-906-16-127

US-08-906-16-127

US-08-906-16-127

US-08-906-16-127

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US-08-999-689A-25
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                                                                                 OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Sequence Seq
US-09-189-035-2 US-09-382-086-2 US-09-252-991A-30173 US-09-252-991A-20017 US-09-154-802-1 US-09-373-029-1 US-09-252-991A-29543 US-09-252-991A-29543 US-09-252-991A-2951 US-09-252-991A-2951 US-09-134-001C-5241 US-09-134-001C-5241 US-09-107-532A-7127 US-09-107-532A-7127 US-09-107-532A-7127 US-09-252-991A-21539 US-09-252-991A-21539 US-09-252-991A-19154
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FILING DATE: 1999-07-07
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APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Brooding the Same
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100.0%; Pred. No. 1.9e-14;
ive 0; Mismatches 0; Indels
   PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
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PRIOR PLING DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
PILING DATE: 1999-09-15
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Sequence 423, Application US/09905125A
Patent No. 6664376
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 100.
Matches 24; Conservative
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Raton, Dan L.
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CRGANISM: Homo Sapien
US-09-907-794A-423
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APPLICANT:
APPLICANT:
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 310
                                                                                                                                                                                                                                                                    PRIOR PILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-15
PRIOR PLILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
                                         PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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ION NUMBER: US 60/145,698
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Pilvaroff, Ellen
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Gerritsen, Mary E.
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Roy, Margaret Ann
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Mather, Jennie P.
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Best Local Similarity 100.0
Matches 24; Conservative
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Baton, Dan L.
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Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith B.
APPLICANT: Rushlow, Keith B.
APPLICANT: Rushlow, Keith B.
APPLICANT: Rushlow, Genn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLBIC ACID TITLE OF INVENTION: MOLECULES, AND USES THERROF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Sheridan Rose P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 48;
                                                               COUNTRY: Usa

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/485,455D

FILING DATE: 07-UNA-1995

CLASSIFICATION: 434

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REGISTRATION NUMBER: 2618-25-C1-3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION PROPERSIONES:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 amino acids
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MEDIUM TYPE: Ploppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,130C
FILING DATE: 07-JUN-1995
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
RESTEXENCE/DOCKET NUMBER: 2618-25-C1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches
3: Sheridan Ross P.C.
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/08482130C
Patent No. 5962257
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                               Denver
: Colorado
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 ADDRESSEE:
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APPLICANT: Rushlow, Keith B.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Prank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FIER PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.9
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GENERAL INFORMATION:
               Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
   Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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; ORGANISM: Homo Sapien
US-09-902-775A-423
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 65, Application US/08484211C
Patent No. 5972645
GENERAL INFORMATION:
APPLICANT: Grave, Robert B.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Fu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: PLEA PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                         Length 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 80203

COMPUTER 180203

COMPUTER: Ploppy disk

COMPUTER: IPA PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,211C

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTOMEY/AGENT INFORMATION:

NAME: CONNell, Gary J.

REGISTRATION NUMBER: 32,020

RESTRENCE/DOCKEY NUMBER: 2618-25-C1

TELEPAN: (302) 863-9700

TELEPAN: (303) 863-9700

TELEPAN: (303) 863-0223

INFORMATION POR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 amino acids
                                                                                                                                                                                                         Score 8; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1700 Lincoln Street, Suite 3500 CITY: Denver STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3...
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                     Query Match 2.6%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 3.1
Matches 8; Conservative 0; Mismatches
(303) 863-9700
               TELEFAX: (303) 863-0223
INPORMATION POR SEQ 1D NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-130C-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-484-211C-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan
                                                                                                                                                                                                                                                                                        252 VLIVLAVI 259
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US-08-484-211C-65
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Sequence 65, Application US/08906769

FREERLA INFORMATION:

JAPLICANT GLINE, RADIO SALE B.

APPLICANT GLINE, SALE B.

APPLICANT GLINE, SALE B.

APPLICANT GLINE STANDING, KALIE B.

APPLICANT GLINE STANDING, KALIE B.

APPLICANT GLINE STANDING THE PROTESSE PROTEINS, NUCLEIC ACID ITTLE OF INVESTIONS: PARTY B.

APPLICANT GLINE SALVES AND USES THERROP CONTRESS THOREOF CONTRESS AND USES THERROP CONTRESS AND USES AND USES THERROP CONTRESS AND USES AND USES THERROP CONTRESS AND USES AND USE AND USES AND UNDERSON AND UNDERSON AND USES AND USES AND USES AND UNDERSON AND USES AND USES AND USES AND USES AND UNDERSON AND UNDERSON AND USES AND USES AND UNDERSON AND USES AND USES AND UNDERSON AND UNDERSON AND USES AND UNDERSON AND UNDERSON AND USES AND USES AND UNDERSON AND USES AND USES AND USES AND USES AND USES AND UNDERSON AND USES AN
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RESULT 7

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US-08-485-443B-65; Application US/08485443B
; Sequence 65, Application US/08485443B
; Patent No. 6146870
; GENERAL INFORMATION:
APPLICANT: Rushlow, Reith B.
APPLICANT: Huncer, Shirley Wu.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Fried Glenn R.
TITLE OF INVENTION: MOLECULES AND USES THEREOF
TITLE OF INVENTION: MOLECULES AND USES THEREOF
MUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%; Score 8; DB 3; Length 48; 100.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 48;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,443B
PILING DATE: US/08/4871ON: TELEPHONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
PIREPAK: 303 863-9700
PIREPAK: MARCHERISTICS:
SEQUENCE CHRARACTERISTICS:
LENGTH: 48 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%; Score 8; DB 3; 100.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Gary J. Comnell
RECISTATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 10 NO: 65:
SEQUENCE CHRACATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                   48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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Best Local Similarity
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GY: linear
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Sequence 55, Application US/08817795

Sequence 55, Application US/08817795

GENERAL INFORMATION:

APPLICANT: Rushlow, Keith B.

APPLICANT: Heath, Andrew W.

APPLICANT: Yamawa, Miles Yamanaka

APPLICANT: Yamawa, Miles Yamanaka

APPLICANT: Yamawa, Miles Yamanaka

APPLICANT: Andrew W.

APPLICANT: Andrew W.

APPLICANT: Stiegler, Ann

TITLE OF INVENTION: NESTATION, AND FLEA PROTECT ANIMALS FROM FLEA

TITLE OF INVENTION: MOLECULES, AND USES THEREOF

NUMBER OF SEQUENCES: 119

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 48;
                                                                                        COUNTRY: USAN
ZIP: 80203
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CORNEIL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/POCKET NUMBER: 32,020
REFERENCE/POCKET NUMBER: 32,020
RECISTRATION NUMBER: 32,020
TELEPHONE: (303) 863-9700
TELEPRAX: (303) 863-9700
TELEPRAX: (303) 863-9700
TELEPRAX: (303) 863-9700
TELEPRAX: (303) 863-9700
TELERAX: (303) 863-9700
TELERAXION FOR SEQ ID NO: 65:
SEQUENCE CHARACTER STICS:
LENGTH: 48 amino acids
""""
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.6%; Score 8; DB 3
Best Local Similarity 100.0%; Pred. No. 3.1
Matches 8; Conservative 0; Mismatches
             1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear; MOLECULE TYPE: protein US-08-906-616-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 VLIVLAVI 259
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STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VLIVLAVI 8
                                                              Colorado
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US-08-817-795-65
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Gaps
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US-09-012-692-65
i Sequence 65, Application US/09012692
; Sequence 65, Application US/09012692
; Batent No. 6214579
; GENERAL INFORMATION:
; APPLICANT: Grieve, Robert B.
; APPLICANT: Wu Hunter, Shirley
; APPLICANT: Frank, Glenn R.
; APPLICANT: Stiegler, Gary
; APPLICANT: Stiegler, Gary
; APPLICANT: Silver, Gary
; TITLE OP INVENTION: FLEA PROTEASE PROTEINS, NUCLBIC ACID
; TITLE OP INVENTION: FLEA PROTEASE THEREOF
; NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan P.
  Silver, Gary
TITLE OF INVENTION: PLEA PROTEASE PROTEINS, NUCLEIC ACID
MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Derver
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/012,431
PILING DATE: 33-3an-1998
CLASSIPICATION > 40hcnom>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION ONTO ATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: CONNEIL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%; Score 8; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                             ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                    NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                    STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-012-431-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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    Gaps
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                                                                                                                                                                                                                                                               APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Rotth B.
APPLICANT: Rushlow, Raith B.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Gaines, Suite JSOO
CITY: Denver
STATE: Colorado
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIPICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: COMPOLIA GATY J.
REGISTRATION NUMBER: 2618-25-C2
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION INPORMATION:
TELECOMMUTICATION OF SOTION
THE FRENCH COMPUTER: 2619-25-C2
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100.0%; Pred. No. 3.1;
trive 0; Mismatches
  0; Mismatches
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US-09-012-431-65
Sequence 65, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
RUBHOW, Keith B.
RUBHOW, Keith B.
WHUNCEY, Shirley
Frank, Glenn R.
Stiegler, Gary
Gaines, Patrick J.
                                                                                                                                                                                                     Sequence 65, Application US/08639075A; Patent No. 6150125; GENERAL INFORMATION: APPLICANT: Grieve, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS: LENGTH: 48 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 8; Conservative
  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                252 VLIVLAVI 259
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                                                                           1 VLIVLAVI 8
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Matches
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TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
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Best Local Similarity
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APPLICANT: Rushlow, Keith E.
APPLICANT: Nu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Hower, Gary
APPLICANT: Silver, Silver, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,613
FILING DATE:
  OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6%; Score 8; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches
                                                                                          FILING DATE:
CLASSIFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-ARR-1996
ATTONNEY, AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFREENCE/DOCKET NUMBER: 2618-25-C2
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/08906613; Patent No. 6232096; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ 1D NO: 65:
SEGURENCE CHARACTERISTICS:
LENGTH: 48 emino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-012-692-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 VLIVLAVI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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STATE: Colorac
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-906-613-65
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APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith B.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Wiles Yamanaka
APPLICANT: Yamaka, Wiles Yamanaka
APPLICANT: Yamaka, Miles Yamanaka
APPLICANT: Yamaka, Miles Yamanaka
APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: Bale, BROTEASE INHIBITORS AND
ITITLE OF INVENTION: PROTEASE VACINES TO PROTECT ANIMALS FROM FLEA
ITITLE OF INVENTION: MOLECULES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6%; Score 8; DB 5;
100.0%; Pred. No. 3.1;
                                                                                                                                                                                    2.6%; Score 8; DB 3
100.0%; Pred. No. 3.1
trive 0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 65, Application PC/TUS9514442A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
INFORMATION POR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                            2.6

Query Match
Best Local Similarity 100.
Matches 8; Conservative
TYPE: amino acid
TOPOLOGY: linear
HOLECULE TYPE: protein
US-08-906-613-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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Search completed: June 15, 2004, 11:13:22 Job time : 17.5 secs

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Sequence Sequence Sequence

score:

Title: Perfect

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Database :

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Sequence 18, Application US/10410842A
| Sequence 18, Application US/10410842A
| Publication No. US20030236396A1
| GENERAL INFORMATION:
| APPLICANT: Fasel et al
| TITLE OF INVENTION: SECRETORY SIGNAL SEQUENCES AND USES THEREOF
| PILE REFERENCE: 29964/37635A
| CURRENT APPLICATION NUMBER: US/10/410,842A
| CURRENT PILING DATE: 2002-04-09
| PRIOR APPLICATION NUMBER: US 60/371,029
| PRIOR PILING DATE: 2002-04-09
| WUMBER OF SEQ ID NOS: 69
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 18
| LENGTH: 238
| TYPE: PRT
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US-09-904-786-423
US-09-906-646-423
US-09-905-700-423
US-09-903-786-423
US-09-903-786-423
US-09-903-786-423
US-09-904-119-423
US-09-904-136-423
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US-09-905-613-423
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US-09-905-613-423
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100.0%; Pred. No. 4.2e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 PRPHYSWYRNDVPLPTDSRANPRF 190
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; Sequence 413, Application US/09909320
; Sequence 413, Application US/09909320
; GENERAL INFORMATION:
    APPLICANT: Genentech, Inc.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.7
Best Local Similarity 100.
Matches 24; Conservative
    ) ORGANISM: Homo sapiens
US-10-410-842A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-410-842A-18
      167
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                                                                                                                                                June 15, 2004, 11:10:00 ; Search time 39 Seconds (without alignments) 2239.361 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423, A Sequence 423, Sequ
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                                                                                                                                                                                                                                                       310
1 MALSRRLRLRLYARLPHFFL......VNYIRTSEBGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB_POP:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB_POP:*

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11: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

13: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

14: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

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16: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

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16: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

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17: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*

18: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.POP:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158786
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-909-908-423
US-09-902-813-423
US-09-907-824-423
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US-09-907-813-423
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                                                                                                                                                                                                                                                                                                                                                                                1158786 seqs, 281726120 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                        US-09-524-531C-13
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Maximum DB seq length: 200000000
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Match Length
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Result

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JS-09-909-088B-423

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PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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PRIOR PPLICATION NUMBER: PCT/USOU/04414
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-26
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OR APPLICATION NUMBER: PCT/US00/04114
OR PILING DATE: 2000-02-22
OR PILING DATE: 1999-07-07
OR PILING DATE: 1999-07-07
OR PILING DATE: 1999-07-07
OR APPLICATION NUMBER: US 60/145,698
OR APPLICATION NUMBER: US 60/146,222
OR FILING DATE: 1999-07-28
OR PILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
OR APPLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/909,320 CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                          Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth, J
                                                           Gerber, Hanspeter
Gerritsen, Mary E.
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Best Local Similarity 100.0
Matches 24; Conservative
                                   Wei-Qiang
Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 10466-14
                                                                                                                                     Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo Sapien
US-09-909-320-423
                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT
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APPLICANT: FROIL, MICROIDER F.
APPLICANT: Stewart, Timcholm B.
APPLICANT: Stewart, Timcholm A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBYCE: 10466-14
CURRENT FILLEND DATE: 2001-07-18
FRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: DS 60/145,698
RRIOR APPLICATION NUMBER: US 60/145,698
RRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
Sequence 423, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P
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Botstein, David
Desnoyers, Luc
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Sequence 423, Application US/09902853 Publication No. US20020192659A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Paoni, Nicholas F.
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Mather, Jennie P.
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Best Local Similarity 100.0
Matches 24; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Baton, Dan L.
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ORGANISM: Homo Sapien
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/095,291A
CURRENT APPLICATION NUMBER: 2001-07-12
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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100.0%; Pred. No. 5.4e-15;
ive 0; Mismatches 0; Indels
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Sequence 423, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
Gerber, Hanspeter
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Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 100.0
Matches 24; Conservative
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Baton, Dan L.
                       LENGTH: 310
TYPE: PRT
ORGANISM: Homo Sapien
                                                                         j ORGANISM: Homo
US-09-909-088B-423
SEQ ID NO 423
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERRNCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT APPLICATION NUMBER: 2001-07-10
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLING DATE: 1999-07-28
PRIOR APPLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLING DATE: 1999-09-08
FRIOR APPLICATION NUMBER: PCI/US39/A0303

PRIOR APPLICATION NUMBER: PCI/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30919

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-26

PRIOR FILING DATE: 1999-12-36

PRIOR FILING DATE: 1999-12-36

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 10
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US-09-907-841-423
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
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PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-30
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PRIOR PILING DATE: 2000-01-05
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CURRENT APPLICATION NUMBER: US/09/907,824
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary B.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Inc
APPLICANT: Baton, Dan L.
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PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PPLICATION NUMBER: PCT/USS9/2814
PRIOR PPLICATION NUMBER: PCT/USS9/28113
PRIOR APPLICATION NUMBER: PCT/USS9/28113
PRIOR APPLICATION NUMBER: PCT/USS9/28564
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/USS9/30095
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-04
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USS9/30911
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
PRIOR FILING DATE: 2000-12-16
PRIOR PLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USOO/04414
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
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PRIOR PLING DATE: 1999-09-09
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Bacno, Dan L.
APPLICANT: Bacno, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Follong, Sherman
APPLICANT: Gao, Wei-Olang
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Grimaldi, Christopher J.
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Best Local Similarity 100.09
Matches 24; Conservative
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| APPLICANT: WOOD, WILLIAMS | F. PLUCKEY | APPLICANT: WOOD, WILLIAMS | I. ALGER | APPLICANT: WOOD, WILLIAMS | I. ALGER | APPLICANTION | APPLICANTION | ACCIDED | APPLICANTION | ACCIDED | APPLICANTION | ACCIDED | ACCID
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7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels
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8.09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INPORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                          Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                   Roy, Margaret Ann
Stewart, Timothy A.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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ORGANISM: Homo Sapien
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APPLICANI:

AUCOS, NILISANI, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REPREEENCE: 10466-14

CURRENT PILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
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Publication No. US20030003530A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Bllen
Fong, Sherman
Gao, Wei-Glang
Gerber, Hanapeter
Gerritsen, Mary B.
      Hillan, Kenneth, J.
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Hillan, Kenneth, J
                                                                                                              Pan, James
Paoni, Nicholas F.
                                            Kljavin, Ivar J.
Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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CORGANISM: Homo Sapien
US-09-907-841-423
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167 PRPHYSWYRNDVPLPTDSRANPRF 190
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24; Conservative
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APPLICANT:
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Matches
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PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-16
CURRENT FILING DATE: 2001-07-16
PRIOR PELICATION NUMBER: 09/665,350
PRIOR PELICATION NUMBER: 09/665,350
PRIOR PELICATION NUMBER: 05/0414
PRIOR PELING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-38
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-00-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-13-30
                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rather, Jennie P.
Pan, James
Pani, Nicholas P.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                      Ferrara, Napoleone
Filvaroff, Bllen
Fong, Sherman
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                                                                                                                                                                                                                                          Gerber, Hanspeter
   Botstein, David
                                                                                                                                                                                                             Wei-Qiang
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ORGANISM: Homo Sapien
US-09-906-742-423
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Best Local Similarity
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APPLICANT:
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"An Mary E. "

"All An Mary E. "

"Hill An Markin L. "

"All Annia F. "

"Annia F. "

Sequence 423, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          Perrara, Napoleone
Pilvaroff, Ellen
                                                                                                                                                Ashkenazi, Avi
Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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100.0%; Pred. No. 5.4e-15;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR PELING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
                                    PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PLING DATE: 1999-12-20
                    PPLICATION NUMBER: PCT/US99/28214
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; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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FILING DATE: 1999-10-05
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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Best Local Similarity 100.0
Matches 24; Conservative
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILS REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-05-27
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                                                                                                                                                                                                                                                                                                  Length 310;
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100.0%; Pred. No. 5.4e-15;
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APPLICATION NUMBER: PCT/US99/21547
PILING DATE: 1999-09-15
PILING BATE: 1999-09-18
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 423
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
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APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20030027145A1
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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                                                                                                                                                                                                                        ORGANISM: Homo Sapien
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US-09-907-613-423
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                                                                                                                                                                            LENGTH: 310
TYPE: PRT
                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT:
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Gaps

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### PRELICANT: WILLIAMS: P. BLCKEY
### APPLICANT: WOOd, Williams, I.
### TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
### TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
### TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
### CURRENT PILLIA DATE: 2001-07-12
### CURRENT PILLIA DATE: 2000-09-18
### PRIOR FILLING DATE: 2000-09-18
### PRIOR FILLING DATE: 2000-03-22
### PRIOR FILLING DATE: 1090-02-22
### PRIOR FILLING DATE: 1090-03-03
### PRIOR FILLING DATE: 1090-10-03
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Publication No. US20030036061A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-859-423
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US-09-909-204-423
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APPLICANT:
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7.7%; Score 24; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1990-09-08
PRIOR PILING DATE: 1990-09-13
PRIOR PILING DATE: 1990-09-15
PRIOR PILING DATE: 1990-10-05
PRIOR PILING DATE: 1990-10-05
PRIOR PILING DATE: 1990-11-20
PRIOR PILING DATE: 1990-12-02
PRIOR PILING DATE: 1990-12-02
PRIOR PILING DATE: 1990-12-02
PRIOR PILING DATE: 1990-12-20
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Publication No. US20030036060A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bostetin, David
APPLICANT: Bestetin, David
APPLICANT: Batton, David
APPLICANT: Batton, David
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Bllen
Fong, Sherman
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Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-423
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US-09-904-859-423
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APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
PILE REPERENCE: 10466-14
Sequence 423, Application US/09904820
Publication No. US20030036094A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Pilvaroff, Ellen
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Gerritsen, Mary B.
Goddard, A.
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Mather, Jennie P.
Pan, James
                                                                                           APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                           APELICANT: Pani, James
APELICANT: Pani, James
APELICANT: Roy, Margaret Ann
APELICANT: Stewart, Timothy AP
APELICANT: Stewart, Timothy AP
APELICANT: Mulliama, P. Mickey
APELICANT: Williama, P. Mickey
APELICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE OF APELICATION NUMBER: PCT/US00/04414
FRIOR APELICATION NUMBER: PCT/US00/04414
FRIOR APELICATION NUMBER: PCT/US09/2054
FRIOR APELICATION NUMBER: PCT/US09/2054
FRIOR APELICATION NUMBER: PCT/US09/2054
FRIOR APELICATION NUMBER: PCT/US09/2054
FRIOR PLILING DATE: 1999-00-15
FRIOR PLILING DATE: 1999-00-15
FRIOR PLILING DATE: 1999-10-15
FRIOR PLILING DATE: 1999-10-15
FRIOR PLILING DATE: 1999-11-20
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100.0%; Pred. No. 5.4e-15;
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
               Gerritsen, Mary E.
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Mather, Jennie P.
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Best Local Similarity 100.0
Matches 24; Conservative
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ORGANISM: Homo Sapien
US-09-909-204-423
                                                                                                                                                                                                                                                                                        Pan, James
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PILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 1900-07-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-1
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RESULT 15 US-09-904-820-423

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; ORGANISM: Homo Sapien
US-09-904-820-423
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ö 0; Gaps Query Match 7.7%; Score 24; DB 10; Length 310; Best Local Similarity 100.0%; Pred. No. 5.4e-15; Matches 24; Conservative 0; Mismatches 0; Indels

167 PRPHYSWYRNDVPLPTDSRANPRP 190
167 PRPHYSWYRNDVPLPTDSRANPRF 190 ઠે g

Search completed: June 15, 2004, 11:14:52 Job time : 39 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

June 15, 2004, 11:06:35; Search time 14 Seconds (without alignments) 2129.955 Million cell updates/sec

US-09-524-531C-13

Title: Perfect score:

1 MALSRRIRLRLYARLPHFFL.......VNYIRTSEEGDFRHKSSFVI 310 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283366 segs, 96191526 residues

Searched:

0 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		d			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
-	8	2.6	146	7	F70313	hypothetical prote
8	60	5.6	204	~	A89919	conserved hypothet
e	60	2.6	208	~	D83431	type III export pr
4	60	2.6	506	~	T02400	probable beta-gluc
v	8	5.6	959	7	B85276	hypothetical prote
9	7	2.3	118	٦	GIYC	gene 1 protein - S
7	7	2.3	128	~	CB3448	
80	7	2.3	137	~	B41047	exsB protein - Pse
σ	7	2.3	137	7	E83433	exoenzyme S synthe
10	7	2.3	173	7	B90241	
11	7	2.3	177	~	E85833	partial probable s
12	7	2.3	177	~	B90988	partial probable s
13	7	2.3	194	7	T28889	hypothetical prote
14	7	2.3	208	7	T03627	GTP-binding protei
15	7	2.3	208	~	T01588	GTP-binding protei
16	7	2.3	214	~	T47268	
17	7	2.3	224	~	D71915	hydrogenase, cytoc
18	7	2.3	232	~	S60984	
19	7	2.3	246	7	P91238	44
20	7	2.3	246	~	B86086	PTS system, fructo
21	7	2.3	249	7	G84224	
22	7	2.3	255	~	B72474	hypothetical prote
23	7	2.3	267	~	B63705	phosphonates trans
24	7	2.3	269	Н	C69651	prolipoprotein dia
25	7	2.3	280	~	HB3623	probable chemotaxi
56	7	2.3	287	~	B75159	hypothetical prote
27	7	2.3	322	~	B69009	cation antiporter
28	7	2.3	324	~	T27302	hypothetical prote
29	7	2.3	332	Н	DEBYG1	glyceraldehyde-3-F

glyceraldehyde-3-p probable high-affi glyceraldehyde-3-p	hypothetical prote Liditol 2-dehydro pts system, fructo Richardowylmalate	nitrogen fixation hypothetical prote protein T27G7.16 (	aminotransferase ( MPS permease [impo hypothetical prote	hypothetical prote L-geryl-tRNASec se hypothetical prote
DEBYG2 C72485 S29813	A12360 B84143 H65201	E90533 G83367 H86217	D70110 AG2718 C97500	S75859 A70389 T28118
4 4 4	0000	9000	000	000
332 332 335	337 359	387 402 421	422 429 429	445 452 473
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30 31 32	. W W W V	1 W W W	4 4 4 0 11 4	4 4 4 ሠ 4 ሺ

## ALIGNMENTS

hypochetical protein ag 142 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: OseMay-1998 #sequence\_revision 08-May-1998 #text\_change 04-Mar-2000 C;Accesion: P70313 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Retus: nr F70313
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1.146 cAQF>
A;Cross-references: Gal-RE000675; NID:g2982863; PIDN:AAC06501.1; PID:g2982881; GB:AB0006
A;Experimental source: strain VF5
C;Genetics:
C;Genetics:
C;Superfamily: Aquifex aeolicus hypothetical protein aq\_142

Length 146; 0; Indels Query Match 2.6%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 2.6; Matches 8; Conservative 0; Mismatches

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Gaps

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252 VLIVLAVI 259 ហ 셤 ਨੇ

#### RESULT 2

conserved hypothetcial protein SA1250 (imported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus C.bate: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 02-Jun-2003

C;Accession: A88919
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu M.; A.; Mizutani-Ui, K.; Kabayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-204 «KUR» A;Cross-references: GB:BA000018; PID:g13701215; PIDN:BAB42510.1; GSPDB:GN00149 A;Experimental source: strain N315

C; Genetics

A;Gene: SA1250 C;Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain ho

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hypothetical protein AT4924020 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: B85276
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spri Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A65001; MUID:20083488; PMID:10617198
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C3448
R;Stover. C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Species: Synechococcus sp.
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
R;Cozens, A.L.; Walker, J.B.
J. Mol. Biol. 194, 359-383, 1987
J.Mol. Biol. 194, 359-383, 1987
A;Title: The organization and sequence of the genes for ATP synthase subunits in the cy A;Reference number: S07286; MUID:87311713; PMID:3041005
A;Accession: S10825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-959 <STO>
A;Cross-references: GB:NC_001268; NID:g7269251; PIDN:CAB81320.1; GSPDB:GN00140
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KResidues: 1-118 <COZ-
A;Cross-references: EMBL:X05302; NID:g48009; PIDN:CAA28922.1; PID:g48011
C;Superfamily: gene I protein
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A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein F23812.170
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches
                            Pred. No. 7.7; Mismatches
100.0%; Fre
                                                                          8; Conservative
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                                                                                                                                                                   250 LVVLIVLA 257
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Matches 8; Conserv
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C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Species: Ds-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: D83431
R; Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Pardy, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathothy Ricession: D83431
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Residues: 1-208 cSTO
A; Molecule type: DNA
A; Residues: 1-208 cSTO
A; Rosidues: 1-208 cSTO
A; Ros
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Peb-2001
C;Accession: T02400; P84878
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F411 genomic sequence.
A;Reference number: Z1467
A;Reference number: Z1467
A;Reference number: Z1467
A;Reference number: EMBL/DDBJ
A;Retaus: translated from GB/EMBL/DDBJ
A;Reterence number: Radat20; MUID:20083487; PMID:10617197
A;Reference number: Agadat20; MUID:20083487; PMID:10617197
A;Retaus: translated from GBARTA
A;Retaus: translated from GB/EMBL/DBJ
A;Reference number: A;Reference and analysis of chromosome 2 of the plant Arabidopsis thallana.
A;Reference number: A;Referenc
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Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches
                       Query Match 2.6%; Score 8, DB 2; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                             181 iAGIIGGV 188
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A;Molecule type: DNA
A;Residues: 1-506 <STO>
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2.6%; Score 8; DB 2; Length 506;

Query Match

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partial probable sensor kinase 23235 [imported] - Escherichia coli (strain O157:H7, subi C;Species: Escherichia coli C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 C;Date: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 R;Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayher iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, N;title: Genome sequence of enterohemorrhagic Bscherichia coli O157:H7.
A;Reference number: A885480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
CiAccession: B99988
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Bysawara, N.; Ysaunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
BNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Bscherichia coli 0157:H7 and geno
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: GB:AE006641; NID:g13814083; PIDN:AAK41185.1; GSPDB:GN00155
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100.0%; Pred. No. 34;
tive 0; Mismatches
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100.0%; Pred. No. 33;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 IIGGVLV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 IIGGVLV 251
     7 LRLRLYA 13
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41 LRLRLYA 47
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A; Residues: 1-177 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B90241
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A;Residues: 1-137 <STO>
A;Cross-references: GB:AE004597; GB:AE004091; NID:g9947671; PIDN:AAG05101.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exsB protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 08-Oct-1999
C;Accession: B41047
R;Frank, D.W.; Iglewski, B.H.
J. Bacteriol. 173, 6460-6468, 1991
A;Title: Cloning and sequence analysis of a trans-regulatory locus required for excenzym
A;Reference number: A41047; WUID:92011420; PMID:1655713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E31433
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Baadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Courey, S.; Olson, M.V.
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A;Accession: E83433
A;Status: preliminary
                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <STO>
A;Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AAG04970.1; GSPDB:GN001
A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A,Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exoenzyme S synthesis protein B PA1712 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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*Residues: 1-137 <FRA>
A;Cross-references: GB:M64975; NID:g151217; PIDN:AAA25815.1; PID:g151219
C;Superfamily: Pseudomonas aeruginosa exsB protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                               Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.3%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 27; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                         Ouery Match 2.3%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                       A, Experimental source: strain PAOI
C, Genetics:
A, Gene: sdhC; PA1581
C, Superfamily: succinate dehydroger
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                                                                                                                                                                                                                                                                                                                                                                                                                                       251 WLIVLA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VVLIVLA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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Length 208;

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Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                               187 VNLKSSN 193
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                                                                                                                                                                                          32 VNLKSSN 38
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yMolecule type: DNA
yResidues: 1-208 <STO>
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T03627
GTP-binding protein Rab6 - common tobacco
C; Species: Nicotiana tabacum (common tobacco)
C; Species: Nicotiana tabacum (common tobacco)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C; Accession: 103627
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
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R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.
R; Haizel, T.; Merkle, T.; Turck, F.; Nagy, F.;
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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90988
A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-17 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36297.1; PID:g13362343; GSPDB:GN00154
A;Cross-references: GB:BA1000007; PIDN:BAB36297.1; PID:g13362343; GSPDB:GN00154
A;Cross-references: GB:BA1000007; PIDN:BAB36297.1; PID:g13362343; GSPDB:GN00154
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T14B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T28B89
R;Pavello, T.
submitted to the BMBL Data Library, March 1996
A;Reference number: Z20539
A;Reference number: Z20539
A;Reference number: Z20539
A;Accession: T28889
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 49/2; 104/2; 137/3
C;Superfamily: Caenorhabditis elegans hypothetical protein T14B4.5
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A;Residues: 1-194 «FAV.»
A;Cross-references: EMUBL:U50191; PIDN:AAA91238.1; CESP:T14B4.5
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                             Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 7; DB 2
100.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 GGVLVVL 145
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <ROD:
A;Cross-references: EMBL:AC003672; NID:g3341671; PIDN:AAC27463.1; PID:g3341681
A;Cross-references: EMBL:AC003672; NID:g3341671; PIDN:AAC27463.1; PID:g3341681
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding protein At2g44610 - Arabidopsis thaliana
N;Alternate names: protein F16B22.10
S;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 02-Mar-2001
C;Accession: T01588; F84880
C;Accession: T01588; F84880
S;Edin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A;Reference number: Z14284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 2
A;Introns: 39/3; 63/2; 93/1; 110/2; 160/3
A;Introns: 39/3; 63/2; 93/1; 110/2; 160/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Keywords: GTP binding; membrane trafficking; nucleotide binding; P-loop P;10-125/Domain: translation elongation factor Tu homology <BTU>P;10-125/Domain: uranslation elongation factor Tu homology <BTU>P;12-125/Region: GTP-binding motif A (P-loop)
P;122-125/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: P84880
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                                                                                                   Gapa
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                   Score 7; DB 2;
Pred. No. 39;
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2.3%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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2.3%; Score 7; DB 2,
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches
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10

Bacteria; Cyanobacteria; Chroococcales; Synechococcus. 8 oryctolagus oryctolagus drosophila drosophila bacillus su oceanobacil trichoderma escherichia trypanosoma pyrococcus homo sapien borrella bu rotav 066537 aquifex aeo POB443 synechococc aquifex aeo caenorhabdi saccharomyc escherichia mus musculu bacillus su pseudomonas Saccharomyc Saccharomyc brucella me brucella su mus musculu pseudomonas saccharomyc human rotav June 15, 2004, 11:05:10 ; Search time 10 Seconds . (without alignments) 1614.175 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 310 1 MALSRRIRLRIKLYARLPHPT.......VNYIRTSEGDPRHKSSFVI 310 Description Q92114 Q99210 Q91675 Q91675 Q91675 PP00359 PP0 099770 099771 099771 086275 086274 089617 09628 09628 09189 091199 141681 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues SUMMARIES 1.672 FABATI
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1.675 ATPZ\_SYNP6 EXSB\_PSEAE XLR1\_MOUSE YOZ1\_YEAST Post-processing: Listing first 45 summaries - protein search, using sw model OLIGO Gapop 60.0 , Gapext 60.0 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-524-531C-13 Length DB SwissProt 42:\* Copyright Query 0 Title: Perfect score: Scoring table: Score Word size : OM protein Database : Searched: Sequence: Run on: Result No. 

YC26 WETJA Q58623 methanococc AD1B MOUSE Q87534 mus musculu SYFB_ANASP Q87934 anabaena sp CC16 YEAST P097798 saccharomyc YEGE ECCLI PRAST P097798 saccharomyc YEGE HUMAN P34578 caenorhabdi PRN1 BOVIN P98133 bos cancrhabdi PRN1 MOUSE PRN1 PWAN P35555 homo sapien PRN1 MOUSE CAEL POWN P98134 bos caurus PRN1 MOUSE Q61554 mus musculu PRN1 PIG Q91436 sus scrofa CLR1 HUMAN Q91946 homo sapien	Created) Last sequence update) Last annotation update) AQ_142. Aquificales; Aquificaceae; Aquifex. Aquificales; Aquificaceae; Aquifex.	acterium Agreed through and the Brites content age by ant age by an and the Brites content age by an age b	Score 8; DB 1; Length 146; 7; Pred. No. 1.8; 9; Mismatches 0; Gaps 0; PRT; 118 AA. sequence update) annotation update)
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35 33 33 33 33 33 33 44 44 45 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	75 Th	RA Feldman R.A., Short R. The complete genome acolicus.; acolicus.; CC This SWISS-PROT entry CC The SWISS-PROT entry CC the European Bioinfol CC use by non-profit complied and this strong contines requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities requires a cor send an email to CC entities required and this strong cor send an email to CC entities required and this strong cor send an email to CC entities required and this strong correct and contains a co	Duery Match Best Local Simi Best Local Simi Best Local Simi Suz 252 VLI 252 VLI 252 VLI 252 VLI 254 VLI 264 VLI 264 VLI 264 VLI 265 VL

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STRAIN-ATCC 15692 / PAO1;
STRAIN-E0437337; Pubmed-1094043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                             synthase subunits
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"Cloning and sequence analysis of a trans-regulatory locus reguired
tor excerzyme S synthesis in Pseudomonas aeruginosa.";
J. Bacteriol. 173:6460-6468(1991).
                                               Cozens A.L., Walker J.E.;
The organization and sequence of the genes for ATP synthase subuni
in the cyanobacterium Synechococcus 6301. Support for an
endosymbiotic origin of chloroplasts.";
J. Mol. Biol. 1944:359-383(1987)
-!- PUNCTION: A possible function for this protein is to guide the
assembly of the membrane sector of the ATPase enzyme complex.
                                                                                                                                    -!- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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94 114 POTENTIAL.
118 AA: 13455 MW; 16B76A47F76CC196 CRC64;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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Hydrogen ion transport; CP(0); Transmembrane.
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Pred. No. 15;
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=92011420; PubMed=1655713;
                                     MEDLINE=87311713; PubMed=3041005;
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Nature 406:959-964(2000).
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Best Local Similarity 100.
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                       SEQUENCE FROM N.A.
NCBI_TaxID=1139;
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16-OCT-2001
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Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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STRAIN=CSTBL/6; TISSUE-Eye;
Brunner B., Todt T., Lenzner S., Stout K., Schulz U., Ropers H.-H.,
Kalscheuer V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mue
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Retinoschisin precursor (X-linked juvenile retinoschisis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gehrig A.E., Warneke-Wittstock R., Sauer C.G., Weber B.H.P.; "Isolation and characterization of the murine X-linked juvenile retinoschisis (Rslh) gene."; Mamm. Genome 10:303-307(1999).
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MEDJINES99148018; PubMed=10023077;
Reid S.N., Akhmedov N.B., Piriev N.I., Kozak C.A., Danciger M.,
Farber D.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%; Score 7; DB 1; Length 137;
100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
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; F7367E7AB301C4EA CRC64;
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                                                                                                                                                                                                                                                                                           EMBL; AE004597; AAG05101.1; -. PIR; B41047; B41047. PIR; E83433; E83433.
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137 AA; 14996 MW;
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Best Local Similarity lov...
7; Conservative
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RSI OR R61H OR XLRSI.
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CONFLICT 62
SEQUENCE 137 AA;
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                                                                                                                                                                                                                                                                                                                                                                MEDITIES=97344368; PubMed=9200815; Wigheria A., Rechmann S., Teodoru C., Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C., Schwager C., Paces V., Sander C., Ansorge W.; "DMA sequencing and analysis of 130 kb from yeast chromosome XV."; Yeast 13:655-672(1997).
- I- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-- SIMILARITY: Belongs to the maf family.
                                                                                                                                                                                                     Wiemann B., Rechmann S., Benes V., Voss H., Schwager C., Vlcek C., Stegemann J., Zimmermann J., Erfle H., Paces V., Ansorge W.; "Sequencing and analysis of 51 kb on the right arm of chromosome XV saccharomyces cerevisiae reveals 30 open reading frames."; Veast 12:281-288(1996).
YORINIW OR YOR1237W OR O3237.
Saccharomyces cerevisiae (Baker's yeast).
Shkaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Prolipoprotein diacylglyceryl transferase (RC 2.4.99.-) (Spore germination protein gerP).
LGT OR GERF OR ESU34990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%; Score 7; DB 1; Length 232;
100.0%; Pred. No. 28;
iive 0; Mismatches 0; Indels
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
[2]
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STRAIN=S288c / FY1679;
MEDLINE=97060020; Pubmed=8904341;
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SGD; SO005637; YOR111W.
InterPro; IPR00369; Maf.
Pfam; PP0545; Maf; 1.
TIGRPAMS; TIGR00172; maf; 1.
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034752;
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(See http://www.isb-sib.ch/announce/
      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McKernan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
Froc. Natl. Acad. Sci. U.S.A., 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commert entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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BY SIMILARITY.
4536203CC00E90E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 development (By similarity).
--- SUBCELLULAR LOCATION: Secreted (By similarity)
--- TISSUB SPECIFICITY: Retinal specific.
--- SIMILARITY: Contains 1 P5/8 type C domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOZI YEAST STANDARD; PRT; 232 AA. 0992I0; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 49rpothetical protein YOR111W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score 7; DB 100.0%; Pred. No. 27; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000421; FASB C.
InterPro; IPR008979; Gal bind like.
FASB, FRO0754; FS FB type C; I.
FROSTR; PR0121; FASBC; I.
FROSTR; PS01285; FASBC 1; I.
FROSTR; PS01286; FASBC 2; FALSE_NEG.
FROSTR; PS01286; FASBC 2; FALSE_NEG.
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EMBL, AF084562, AAD21809.1, JOINED.
EMBL, AF084563, AAD21809.1, JOINED.
EMBL, AF084564, AAD21809.1, JOINED.
EMBL, AF084565, AAD21809.1, JOINED.
EMBL, AF084565, AAD21809.1, JOINED.
EMBL, AF084565, AAD21809.1, JOINED.
EMBL, BC046422, AA446422.1, F.
HSSP, P12259, 1CZT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 PFLLLLF 24
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YOZ1_YEAST
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AC Q992ÏO,
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                                                                                                                                                                                                                          MULDILARS DAYAGING TO THE MOSECT I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Baresier L., Brans A., Banon M., Briganel S.C., Bron S., Broutilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A., Bariach S.D., Ramerson P.T., Bariach S.D., Farmerson P.T., Britach S.D., Farmerson P.T., A Benizot F., Deviner K.M., Dusterhoft A., Erlich S.D., Gandier D., T., Glaser P., Goffeau A., Golightly B.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiceh J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., A., Cobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Koetter B., Lardinois S., Lauber J., Lazarevic V., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medigue C., Medigue C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moselt D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Reyrolt G., Rocha B., Rose M., Sadaie Y., Scanlan E., Schleich S., Schroeter R., Tognoni A., Tanaka T., Takahashi H., Takemaru K., Tanaka T., Takahashi H., Takemaru K., Tanaka T., Takahashi H., Takemaru K., Yashudt R., Wedler B., Wedler H., Weitzenegger T., Auters P., Willers P., Willers P., Wedler H., Yamanoto H., Yamanoto K., Yashumoto K., Yashumoto K., Yashukawa H., Danchin A., Wanieri P., Walti A., Yamamoto H., Yamanoto K., Yashumoto K., Yashukawa H.P., Danchin A., Wanieri P., Walti R., Weller B., Weller H., Wahuli H., Wanieri P., Walti R., Weller B., Weller B., Weller B., Walti R., Walti R., Weller B., Walti R., Walti 
                                            Karamata D.;
*Nucleotide sequence of the 300-304 chromosomal segment of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: Transfers the N-acyl diglyceride group on what will become the N-terminal cysteine of membrane lipoproteins.
-1- PATHMAY: Lipoproteins biosynthesis; first step.
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: Belongs to the lgt family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fransferase; Transmembrane; Germination; Complete proteome
SEQUENCE FROM N.A.
Lazarevic V., Soldo B., Rivolta C., Reynolds S., Mauel C.,
                                                                                                                  Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99121; CAB15504.1;
PIR; C69651; C69651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subtilist; BG12611; 1gt.
InterPro; IPR001640; LGT.
Pfam; PF01790; LGT; 1.
ProDom; PD005412; LGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGRPAMS; TIGRODS44; 19
PROSITE; PS01311; LGT;
                                                                                                                                                                   SEQUENCE PROM N.A.
                                                                                                                                                                                          STRAIN=168;
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POTENTIAL. 6D2E00DC07482C68 CRC64;

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30619

236 ; 269 AA;

SECUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NACULE TOWNING THE MEMBRANE-BOUND METHYL-ACCEPTING
CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTANYL METHYL ESTER
RESIDUES IN MCP (BY SIMILARITY).
--- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
= S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
--- SIMILARITY: Contains 1 cheR-type methyltransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                     Gaps
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MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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DOMAIN 10 280 CHER-TYPE METHYLTRANSFERASE.
SEQUENCE 280 AA; 32028 MW; FD2AF1491DDC57FB CRC64;
 Length 269;
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                        091677;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chemotaxis protein methyltransferase 2 (EC 2.1.1.80).
Query Match 2.3%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 33;
ive 0; Mismatches
                                                                                                                                                                                                           PRT; 280 AA
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InterPro, IPR000780, CheR Metranf.
InterPro, IPR001601, Methyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004455; AAG03565.1; -.
PIR; H83623; H83623.
                                                                                                                                                                                                                                                                                                                                                                         Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP01739; CheR; 1.
Pfam; PR03705; CheR N; 1.
PRINTS; PR00996; CHERNTFRASE.
SMART; SM00138; MeTrc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
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Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS50123; CHER;
                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
                                                                          252 VLIVLAV 258
                                                                                                           245 VLIVLAV 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                     Mountain H.A., Korch C.; "TDH2 is linked to MET3 on chromosome X of Saccharomyces cerevisiae."; Yeast 7:873-880(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norbeck J., Blomberg A.; "Gene linkage of two-dimensional polyacrylamide gel electrophoresis resolved proteins from isogene families in Saccharomyces cerevisiae by microsequencing of in-gel trypsin generated peptides."; Electrophoresis 16:149-156(1995).
                                                                            01.AUG-1992 (Rel. 23, Last sequence update)
By ERB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 2 (BC 1.2.1.12) (GAPDH 2)
TDH2 OR GPD2 OR YJR009C OR J1433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Pungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 23-36; 71-76; 80-85; 198-212; 225-231 AND 321-330.
STRAIN=ATCC 38531 / Y41;
MEDLINE-95255188; PubMed=7737086;
                                                                                                                                                                                                                                                                                                                              "Structural comparison of two nontandemly repeated yeast glyceraldehyde-3-phosphate dehydrogenase genes."; J. Biol. Chem. 255:2596-2605(1980).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
de Haan w. Smits P.H.M., Grivell L.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                       331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X60157; CAA42725.1; -.
EMBL; V01301; CAA608.1; ALT_SEQ.
EMBL; X87611; CAA60931.1; -.
EMBL; Z45509; CAA89531.1; -.
PIR; S57024; DEBYG1.
HSSP; P06977; IGAB.
GARMOLLINE; 141845; -.
SWISS-2DPAGE; P00358; YEAST.
COMPLUYEAST-2DPAGE; P00358; -.
                                      PRT;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=80137492; PubMed=6244283;
Holland J.P., Holland M.J.;
                                                                                                                                                                                                                          MEDLINE=92160396; PubMed=1789010;
                                                              (Rel. 23, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase family.
                                      STANDARD;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=4932;
                                                              21-JUL-1986
                                      G3P2 YEAST
P00358;
             RESULT 8
G3P2_YEAST
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AGI ...
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Holland J.P., Holland M.J.;
"The primary structure of a glyceraldehyde-3-phosphate dehydrogenase gene from Saccharomyces cerevisiae.";
J. Biol. Chem. 254:9839-9845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete sequence of a 9037 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII."; Yeast 11:587-591(1995).
                                                                                                                                                                                                                                                   ACTIVATES THIOL GROUP DURING CATALYSIS.

B -> A (IN REF. 4).

3998B6F655APDFC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norbeck J., Blomberg A.; "Incompare the complete of two-dimensional polyacrylamide gel electrophoresis "Gene linkage of two-dimensional from isogene families in Saccharomyces cerevisiae by microsequencing of in-gel trypsin generated peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 31, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3).
TDM3 OR GPD3 OR YGR192C OR G7576.
Saccharowyces crevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharowycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
NGT_TAXID=4932;
SGD; S0003769; TDH2.
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:0005277; C:cell wall (sensu Fungi); IDA.
GO; GO:00054365; P:glyceraldehyde-3-phosphate dehydrogenase (p. InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; I.
Pfam; PF00004; gpdh; I.
Pfam; PF00004; gpdh; I.
Pfam; PR00078; G3PHBRGMASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Putcher B., Kobayashi R., Latter G.I., Schwender E
VOlpe T., Warner J.R., McLiaughlin C.S.;
"Profesin identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c;
MBDLINE-95373283; PubMed=7645350;
Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez M.,
                                                                                                                                                                                                                                                                                                                            Length 331;
                                                                                                                                                                                                                                                                                                                                                                  O; Indele
                                                                                                                                                                                                                                      GLYCERALDEHYDE 3-PHOSPHATE.
                                                                                                                                                                                PROSITE; PSO0071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Multigene family.
INIT_MET 0 0
BINDING 149 149 GLYCERALDEHYDE 3-PHOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 38531 / Y41, and ATCC 44827 / SKQ2N;
MEDLINE=95255188; PubMed=7737086;
                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                   2.3%; Scor.
100.0%; Pred. No. c...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 AA.
                                                                                                                                                                                                                                                                                                                              Score 7; DB 1
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electrophoresis 15:1466-1486(1994)
                                                                                                                                                                                                                                                                                           331 AA; 35715 MW;
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                       176
76
                                                                                                                                                                                                                                                                                                                                                                                                      116 EVVALND 122
                                                                                                                                                                                                                                                                                                                                                                                                                                       26 EVVALIND 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      database.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                                                                                         ACT SITE
CONFLICT
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
G3P3_YBAST
ID G3P3_YEAS
AC P00359;
                                                                                                                                                                                                                                                                                                                                  Query Match
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Enterobacteriaceae; Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 EVVALIND 122
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                                                                                                     SEQUENCE OF 1-31.
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R GermOnline; 141504; -

R GermOnline; 141504; -

R GermOnline; 141504; -

R GermOnline; 141504; -

R SWISS-20PAGE; P00359; -

R GO10009424; TDH3.

R GO; GO100094377; C:cell wall (sensu Fungi); IDA.

R GO; GO:00004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IDA.)

R GO; GO:00004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IDA.)

R InterPro; IPR000173; GAP dhdrogenase.

R InterPro; IPR00044; GAPDH-I.

R PRINTS; PR00079; G3PDHDRGNASE.

R IGRRAMS; TICR01534; GAPDH-I; I.

R PROSTITS; PS00071; GAPDH; I.

R PROSTITE; PS00071; GAPDH; I.
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G3P1_TRIKO STANDARD; PRT; 335 AA.
P17729;
01-77290 (Rel. 15, Created)
01-8EB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
G1ycoraldehydd 3-phosphate dehydrogenase 1 (RC 1.2.1.12) (GAPDH1).
Trichcoderma koningii.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomyceridae; Hypocreales; Hypocreaceae;
          -i- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-i- PATHWAY: Second phase of glycolysis; first step.
-i- SUBGNIT: Homotetramer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- MISCELLANBOORS: THERE ARB THREE GENES FOR G3PDH IN YEAST.
-i- MISCELLANBOORS: THERE ARB THREE GENES FOR G3PDH IN YEAST.
-i- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=M3347;
MEDLINE=93176825; PubMed=8439569;
Watanabe H., Hasumi K., Pukushima Y., Sakai K., Endo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> V (IN REF. 1).
-> D (IN REF. 1).
-> I (IN REF. 1).
CPFE94A335C648B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; NAD; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 7; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 38; ive 0; Mismatches
Blectrophoresis 16:149-156(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 328 1
331 AA; 35615 MW;
                                                                                                                                                                                                                                                                                                                                                                          EMBL, V01300, CAA24607.1; -. EMBL, J01124, AAA88714.1; -. EMBL, X82409, CAA57803.1; -. EMBL, 272977; CAA97218.1; -. PIR, S55870; DEBYG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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176
135
247
328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycolysis; (INIT MET BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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G3P1_TRIXO
G3P1_TRIXO
DT _G3P1_TR
AC _P17729;
DT _01-PRB-DT _28-PRB-DT _28-PRB
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                                                                                                                                                                                                                                                MEDLINE-91031446; PubMed=-2226438;
Sakai K., Hasumi K., Endo A.;
"Two glyceraldehyde-3-phosphate dehydrogenase isozymes from the
"Two glyceraldehyde-3-phosphate dehydrogenase isozymes from the
Koningic acid (heptelidic acid) producer Trichoderma koningii.";
Fur. J. Biochem. 193:195-202(1990).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- BNZYME REGULATION: INHIBITED BY KONINGIC ACID THROUGH THE
INTERACTION OF CYSTEINE RESIDUES WITH KONINGIC ACID EVEN AT VERY
LOW CONCENTRATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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28-FBB-2003 (Rel. 41, Last annotation update)
FTS system, fructose-like-2 IIC component (Phosphotransferase enzyme FIM, C component).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: Second phase of glycolysis; first step.
-i- SUBUNIT: Homotetramer.
-i- SUBCELLUAR LOCATION: Cytoplasmic.
-i- MISCELLANBOUS: THIS PROTEIN IS A KONINGIC ACID
(ANTIBLOTIC)-RESISTANT GAPDH ISOZYME, EXPRESSED BY THE KONINGIC
ANTIBLOTIC)-RESISTANT GAPDH ISOZYME, EXPRESSED BY THE KONINGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 149 GLYCERALDEHYDE 3-PHOSPHATE.
176 176 ACTIVATES THIOL GROUP DURING CATALYSIS.
335 AA, 36121 MW, D3F9A01754281A22 CRC64;
"Cloning of two isozymes of Trichoderma koningii glyceraldehyde-3-phosphate dehydrogenase with different sensitivity to koningic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTIBIOTIC PRODUCTION. SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%; Score 7; DB 1; Length 335; 100.0%; Pred. No. 39; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycolysis; Oxidoreductase; NAD; Multigene family.
INIT MET 0 0
BINDING 149 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 AA
                                                                                                               Biochim. Biophys. Acta 1172:43-48(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dhdrogenase.
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Pfam; PP02800; gpdh; 1.
Pfam; PR02000; gpdh; 1.
TIGRPAMS; TIGR01534; GAPDH; 1.
PROSITE; PS00001; GAPDH; 1.
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PIR, $13205; $13205.
HSSP, P56649; 1DSS.
InterPro; IPR006424; GAPDH-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
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                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcacese;
                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                -i- SIMILARITY: Belongs to the L4B family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
3-isopropylmalate dehydratase large subunit 2 (EC 4.2.1.33)
(Isopropylmalate isomerase 2) (Alpha-IPM isomerase 2) (IPMI 2)
LEUC2 OR PYRAB04370 OR PAB0287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.3%; Score 7; DB 1; Length 374;
100.0%; Pred. No. 43;
ive 0; Mismatches 0; Indels
                                                                                                                                                            STRAIN=427;
Wilson K., Uyetake L., Boothroyd J.C.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0 = 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AA; 41886 MW; 67415135001F9804 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z54340; CAA91141.1; -.
InterPror; IPRO02136; Ribosomal L4/L1E.
Pfan; PF00573; Ribosomal L4; 1.
PROSITE; PS00939; RIBOSOMAL_L1E; 1.
ribosomal protein L4 (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 RRIRIRI 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily.
                     RPL4 OR RPL1
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Q9V1J0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Matches
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                                                                                                                                                                                                                           DISCUSSION OF SEQUENCE.

RELEATED 19446; PubMed=7773198;

RELEATED 3. Reizer A., Saier M.H. Jr.;

RABULINE=55291446; PubMed=7773198;

RA MEDLINE=55291446; PubMed=7773198;

RA RELEATED 3. Reizer B. Saier M.H. Jr.;

RA RELEATED 3. Reizer B. Saier M.H. Jr.;

RA Factor J. Reizer J. Saier M.H. Jr.;

RA Factor 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                Dannels D.L.;
"Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO1427; PTS IIC fructo; 1.
Phosphotransferase system; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 359;
                                                                                            MEDLINE=94089392; PubMed=8265357;
Blattner P.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1CB60AF9FF6CCDAD CRC64;
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(Rel. 33, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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39 POTENTIAL
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BCOGENE; BC11908; frwC.

INLECPPO; IPR003352; Ptrans EIIC.

ILLECPPO; IPR006337; PTS_IIC_fruct.

Pfam; PP02378; PTS_EIIC_i.
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EMBL; AE000469; AAC76931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAGIIGG 248
                                              SEQUENCE PROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 IAGIIGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
176
216
251
251
314
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  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996
01-FEB-1996
15-DEC-1998
                                                                                                                                           Daniels D.L
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P49669;
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RESULT 12 RL4\_TRYBB

22555

Matches

8

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Gaps

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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MEDLINE-21638749; Pubmed=11780052;
MEDLINE-21638749; Pubmed=11780052;
A Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
A Bailey J., Barlow K.F., Bates K.N., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.B., Carder C., Carter N.P.,
A Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Cleapan J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Cleapasn J.C., Clamp M., Clark G., Comnor R.B., Corby N.R.,
Cledg S., Cobley V.B., Collier R.E., Comnor R.B., Corby N.R.,
Coulson A. G., Frankland J.A., Fraser A., French L., Garner P.
A Blington A.G., Frankland J.A., Fraser A., French L., Garner P.
A Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
A Hammond S., Harley J.L., Heath P.D., Ho S., Molheson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knightes A., Laird G.K., Lawlor S.,
A Liehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachie L.J., McLay X., McMurray A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of a novel human gene (SIRP-B2) which encodes a new member of the SIRP/SHPS-1 protein family."; J. Hum. Genet. 45:378-382(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoctation update)
Signal-regulatory protein beta-2 precursor (SIRP-beta-2) (SIRP-b2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Yamaki K., Hayakawa I., Hamaguchi M.;
                                                                                                                                                                                                                            EMBL; ALL

R HAMP: MP 01027; -; 1.

R HAMP: MP 01027; -; 1.

R InterPro; IPR00130; Aconitase N.

InterPro; IPR00151; Cis-H aconitase.

DR PRIMS; PR001415; ACONITASE.

DR PRIGHTS; PR00415; ACONITASE.

DR PROSITE; PS01244; ACONITASE 1: 1.

DR PROSITE; PS01244; ACONITASE 2: 1.

DR PROSITE; PS01244; ACONITASE 2: 1.

DR PROSITE; PS01244; ACONITASE 2: 1.

R HELCINE DISPURED (BY SECTION SULPUR (4FE-4S) (BY SECTION SULPUR (4FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 1; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 323 IRON-SULFUR (4FE-4S) (BY S 380 AA; 41088 MW; B22EEIEGD8016FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.3%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 387 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21036165; PubMed=11185750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRB2 HUMAN STANDARD
Q9P1W8; Q8WWAS; Q9NQK8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 DEITIEL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 DEITIEL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Attachul S.P., Zeeberg B., Buetow K.H., Schaefer C.R., Shular M.K.,
RA Attachul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
RA Eopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh P.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Exapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Atchards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Wiltialon D.K., Mazup D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RA Schnerch Sci. U.S.A., 99:16899-16901(2002).
PHOTION: Probable immunoglobulin-like cell surface receptor.
PHOTION: Probable immunoglobulin-like protein.
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.W., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Trocay A., Tromans A.C., Vaudin M., Wall M., Walliam E., Williams S.A., Whitehead S.L., Mittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       다
                                                                                                                                                                                                                                                                              "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note=No experimental confirmation available;
-!- TISSUR SPECIFICITY: Detected in liver, and at very low levels brain, heart, lung, pancreas, kidney, placenta and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007242; P:intracellular signaling cascade; TAS.
GO; GO:00008285; P:negative regulation of cell proliferation; TAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9P1W8-2; Sequence=VSP_007027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9P1W8-3; Sequence=VSP_007028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9P1W8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB042624; BAA95692.1; -.
EMBL; AL138804; CAC00474.1; -.
EMBL; BC020629; AAH20629.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:15757; SIRPB2.
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R InterPro; IPRucoccons
R Pfam; PP00047; ig; 3.
DR SMART; SM00407; ig; 3.
DR SMART; SM00407; ig; 3.
DR SMART; SM00407; iGv. 1.
DR SMART; SM00407; iGv. 1.
DR RAPE; SM00406; iGv. 1.
DR ROSITE; PS50835; iG LICKE; 3.
DR ROSITE; PS50835; iG LICKE; 3.
RW Repeat; Signal; Transmembrane; Immunoglobulin domain; Glycoprotein; KW Alternative splicing.
FT Signal. 29 387 SIGNAL-REGULATORY PROTEIN BETA-2.
FT CHAIN 29 387 SIGNAL-REGULATORY PROTEIN BETA-2.
FT TRANSMEM 361 383 CTTOPLASMIC (POTENTIAL).
FT TRANSMEM 361 387 CTTOPLASMIC (POTENTIAL).
DOMAIN 384 387 CTTOPLASMIC (POTENTIAL).
1G-LIKE C1-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETAIN-ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Dougherty B., Tomb J.-F., Pleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
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COPACTOR: Pyridoxal phosphate (By similarity).

SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent aminotransferases. Csd subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A -> V (IN REF. 2).
L -> S (IN REF. 2).
F7F20C9F96E0E64B CRC64;
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N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
Missing (in isoform 2).
/FTId=VSP_007027.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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Probable cysteine desulfurase (BC 4.4.1.-).
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100.0%; Pred. No. 44;
ive 0; Mismatches
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Best Local Similarity luv.
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387 AA;
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CARBOHYD
CARBOHYD
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CSD_BORBUL
CSD_BORBUL
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DT 16-0
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completed: June 15, 2004, 11:10:30

Search completed: Job time: 11 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                Interpro; IPR000192; Aminotrans_V.
Pfam; PF00266; aminotran 5; 1.
PROSITE; PS00595; AA_TRANSPER CLASS_5; 1.
Lyase; Pyridoxal phosphate; Complete proteome.
BINDING 235 235 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 422 AA; 48124 MW; 0D37CB39059C2EDD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 422;
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.3%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                       EMBL; AE001121; AAC66472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 NIAGIIG 247
                                                                                                                                                                                           PIR; D70110; D70110.
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                                                                                                                                                                                                             HSSP; P77444; 1JP9
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# <sub>%</sub>

us-09-524-531c-13.oli.rspt

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

June 15, 2004, 11:05:50; Search time 36 Seconds (without alignments) 2716.962 Million cell updates/sec

US-09-524-531C-13

310 1 MALSRRIRLRLYARLPHFFL........VNYIRTSEEGDFRHKSSFVI 310 Perfect score:

Sequence:

Gapop 60.0 , Gapext 60.0 01160 Scoring table:

1017041 seqs, 315518202 residues

1017041 Total number of hits satisfying chosen parameters:

0

Word size :

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

ep\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\*
sp\_phage:\* unclassified: \* vertebrate:\* SPTREMBL 25:\*
: sp\_archea:\*
: sp\_bacteria:\* sp plant:\*
sp rodent:\* virus:\*  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

bacteriap: \*

Bp archeap:\*

# STRAMARTES

	Description	Q9epk4 mus musculu	Q9dlm9 mus musculu	Q9d8b7 mus musculu	Q8bt59 mus musculu	Q96fll homo sapien	Q9bx67 homo sapien	Q8wwl8 homo sapien	Q8rqg2 bacillus ce	Q8i8s1 anopheles g	Q8azh5 rabbit hemo	Q99u70 staphylococ	Q8nwr5 staphylococ	Q8csll staphylococ	P95439 pseudomonas	Q9i313 pseudomonas	Q81r03 bacillus an
SUMMARIES	a ID	11 Q9BPK4	11 Q9D1M9	11 Q9D8B7	11 Q8BT59	1 Q96FL1	1 Q9BX67	1 QSWWL8	2 Q8RQG2	5 Q818S1	L2 Q8AZH5	16 Q99U70	16 QBNWR5	16 Q8CSL1	2 P95439	16 091313	16 Q81R03
	* Query Match Length DB	310	310	310	64	309	310	355	95	131	165	204	204	204	206	208	215
,	Query Match	81.6	79.0	49.0	20.6	7.7	7.7	7.7	2.6	5.6	5.6	5.6	5.6	2.6	5.6	2.6	2.6
	Score	253	245	152	64	24	24	24	<b>6</b> 0	<b>6</b> 0	80	60	80	80	8	80	<b>&amp;</b>
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Q81dy6 bacillus ce Q9xy46 ctenocephal O818d9 entamoeba h	Ognia6 corynebacte		Q7w6k5 bordetella	Q8xkw0 clostridium		O22987 arabidopsis	Q84th9 arabidopsis	Q8t7m0 bombyx mori	Q81bf4 bacillus ce			Q8gaf5 arthrobacte	stx2		œ					Q7tfd7 rhesus cyto	Q93hq4 streptococc	Q89h27 bradyrhizob		Q83ag2 coxiella bu
5 Q81DY6 Q9XY46 Q818D9	5 QBNLA6	6 Q7WIH9	6 Q7W6K5	OBXXW0	0 064879	0 022987	O Q84TH9	Q8T7M0	5 Q81BF4	Q8IABS	Q8N185	OBGAPS	Q8SC57	Q7X345	Q7Y2N4	2 Q99GX8	O QBLPP4	O QBGXY9	0 Q9FB08	2 Q7TFD7	093Н04	5 Q89H27	5 Q913D7	5 Q83AG2
215 16 246 5	324 16	443 16	٦.	443 462 10	506 1	959 1	959 1	1005 5	1065 10	65 5	67 4	68 2	85 9	85 9	85 9	85 13	92 1	92 1	95 1	115 13	121 2	126 10	128 16	133 1(
999	9.0	9.	9.0	9 9	9.6	5.6	2.6	5.6	5.6	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3
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119	285	7 7 7	23	∆ C/	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CSTBIL65; STAIN-61; TISSUE=Embryo;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Yehkuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kankawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Baralov B., Kochiwa H.,

Ruehl P., Lewis S., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Susuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Masbina J., Mazzarelli J., Kombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.; "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI\_TaxID=10090; Q9BPK4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
JAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK. Pamily?"; Curr. Top. Microbiol. Immunol. 251:91-98(2000). PRT; 310 AA. PRELIMINARY; [1] SEQUENCE FROM N.A. PubMed=11036763; Q9EPK4 RESULT 1 Q9EPK4 

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1110002N23Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 SQTSDPRIEWKKIQDGQTTYVYPDNKIQGDLAGRIDVPGKISLRIWNVTRSDSAIYRCEV 117
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STRAIN=CSTBL/6J; TISSUB=Mesonephros;
MBDLINE=22354683; PubMed=1246681;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs.";
Nature 420:563-573 (2002)
EMBL; AJ300304; CAC20704.1; --
EMBL; AR013165; BAB28683.1; --
EMBL; BC024357; AAH24557.1; --
EMBL; BC024357; AAH24557.1; --
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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81.6%; Score 253; DB 11; Length 310;
Best Local Similarity 100.0%; Pred. No. 1e-264;
Matches 253; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
1110002N23Rik protein.
JCAM3 OR JCAM2 OR 111002N23RIK.
Mus musculus (Mouse).
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InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 2.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Kidney;
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Q9D1M9;
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0901M9
1D 0001
AC 09011
DT 01-J
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MEDLINE=2108566); PubMed=1121781;

KANDLINE=2108566); PubMed=1121781;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Pukulashi Y., Konno H., Adachi J., Pukuda S.,

Azawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Azawa K., Mareuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadora K., Mareuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadora K., Mareuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

RA Sakai K., Okido T., Puruno M., Ann H., Baldarelli R., Barsh G.,

RA Bake J., Boffeelli D., Bojunga N., Carninci P., de Bonaldo M.P.,

Brownstein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M.,

Brownstein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M.,

Brownstein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M.,

Kyons P., Marchiomi L., Mashima J., Mazzarelli J., Mombaerte P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

RA Sazuki H., Toyo-oka K., Wang K.H., Wahita Y., Kawaji H., Kohtsuki S.,

Hayashizaki S.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 VALNDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRND 177
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Nature 409:685-690(2001).
Mature 409:685-690(2001).
InterPro; IPR007110; 19-1ike.
InterPro; IPR003598; 19_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=CS7BL/6J; TISSUE=Small intestine;
MEDLINE=21085660; PubMed=11217851;
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60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK017692; BAC25526.1; -.
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SEQUENCE
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Q9BX67
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Q96FL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQTSDPRIBWKKIQDGQTTYVYFDNKIQGDLAGRIDVPGKTSLRIWNVTRSDSAIYRCEV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHXDDSGQYYCIASNDAGAARCEGQDMEV
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 23, Last annotation update)
Junction cell adhesion molecule 3 (Fragment).
Buks musculus (Mouse).
Buksryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. McBI_TaxID=10090;
                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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STRAIN-C57BL/6J; TISSUE-BOdy;
MEDLINE-22354683; PubMed=12466851;
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EMBL; AK0068187; BAB25519.1; -.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.
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Best Local Similarity
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Q8BT59;
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08BT59
1D 08BT69
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                                                                                                                                                                                                   1 GGVLVVLIVLAVITWGICCAYRRGCFISSKQDGBSYKSPGKHDGVNYIRTSBBGDFRHKS
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule 3 precursor (Junctional adhesion
molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
FLJ90288) (Hypothetical protein FLJ90828).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                        Length 64;
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100.0%; Pred. No. 5.8e-17;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUL.2001) to the EMBL/GenBank/DDBJ databases. EMBL; EC10699, AMH10690.1; -. InterPro; IPR007110; Ig-11ke. InterPro; IPR0071598; Ig_c2. SWART; SMO047; ig; 2. SWART; SMO0408; Ig_c2. I. PROSITE, PS50835; IG_LIKE; 2.
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64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein (Fragment)
Homo sapiens (Human)
                                                     20.6%; Score 64; DB 11; I
100.0%; Pred. No. 7.3e-61;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                Matches 64; Conservative
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                                                                                Local Similarity
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heart and identification of a candidate gene, JAM3, expressed during
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les 8; Conserv
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Xu P., Smith D.P.;
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SEQUENCE
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Q8RQG2;
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Q818S1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                          Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.; "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM family members.";
                                                                                                                                            SEQUENCE FROM N.A. Abhason-leger C., Lamagna C., Ozaki H., Kita T., *Junctional adhesion molecules (JAMs) and interendothelial
                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suziki Y., Nagai K., Sugano S., Ishli S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
"Characterization of Junctional Adhesional Molecule-3 on Human
Platelets: A New Member of Immunoglobulin Superfamily.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 24; DB 4; Length 310; 100.0%; Pred. No. 5.9e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Hattori A., Okumira K., Iwayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF356113 ARX27211.;
EMBL; AA344411; CAC69845.1;
EMBL; AA44648; AAX2025.1;
EMBL; AR4464769; BAC11195.1;
EMBL; AK074769; BAC11195.1;
InterPro; IPR001110; Ig-like.
               "Cloning of Human Junctional Adhesion Molecule 3.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 310 AA; 35020 MW; CB39ADF33EA1DAB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 355 AA
  Cunningham S.A., Arrate M.P., Tran T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 PRPHYSWYRNDVPLPTDSRANPRF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Junction adhesion molecule 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG LIKE; 2.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                     SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A.
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01-MAR.-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Odorant-binding protein G.38B.a.
Anopheles gambiae (African malaria mosquito).
Bukaryota; Metazoa; Arthopoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NEI_TAXID-7165;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                              CHAIN 76 355 JUNCTION ADHESION MOLECULE 3. SEQUENCE 355 AA; 39602 MM; 8B1577DEA7B1D4P9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishizawa M., Itoi Y., Ito S., Inoue M.; "Genes induced by glycine in Bacillus cereus."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 92;
cardiogenesis.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable NAD(P)H-flavin oxidoreductase (Fragment).
                                                                                                                                                                                                                                                                                                                                                              Query Match
7.7%; Score 24; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB083554; BAB88982.1; -.
GO; GO:0016491; P:oxidoreductase activity; IRA.
GO; GO:006618; P:electron transport; IRA.
FinarPro; IPR000415; Nitroreductase.
Ffam; PF00881; Nitroreductase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6%; Score 8; DB 2; ilarity 100.0%; Pred. No. 3.9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 PRPHYSWYRNDVPLPTDSRANPRF 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                  EMBL, AJ416101, CAC94776.1, -
Genew, HGNC.15532, JAM3.
InterPro, IPR00710; Ig-like.
InterPro, IPR003598; Ig-22.
                                                                                                                                                             Pfam; PF00047; 19; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 iAGIIGGV 188
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SEQUENCE 204 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus."
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QBCSL1
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Portejole Y., Rasschaert D.;
Phylogenetic analysis of rabbit haemorrhagic disease virus in France
between 1993 and 2000, and the characterisation of RHDV antigenic
     "Identification of distinct families of odorant-binding in the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothecial protein (Hypothetical protein SAV1417).
SAV1417 OR SA1250.
Staphylococcus aureus (strain Muso / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                of Anopheles gambiae.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY146730.
GO, GO:0005549; P:odorant binding; IRA.
GO; GO:0006810; P:transport; IRA.
InterPro: IPR006170; PBP GOBP.
Pfam; PP01195; PBP GOBP. 1.
SEQUENCE 131 AA; 14884 MW; FC7D52E9740E2A64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AA; 16991 MW; 9A6E06A848F69ED8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Capsid protein (Fragment).
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Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.6%; Score 8; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches
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MEDLINE=22422426; PubMed=12536296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Virol. 148:65-81(2003).

EMBL, AJ535102; CAD59257.1; -.

InterPro, IPR004005; Calici_coat.

Pfam, PP00915; Calici_coat.

NON TER.
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IGGVLVVL 14
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NCBI_TaxID=11976;
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QBAZHS;
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98AZH5
AC QBAZH
AC QBAZH
DT 01-MA
DT 01-MA
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OC VITUS
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MEDLINE=21111952; Pubhed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
Whole genome sequencing of meticillin-resistant Staphylococcus
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MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Nagai Y., Takeuchi F., Kuroda M., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
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100.0%; Pred. No. 8.2;
ive 0; Mismatches 0; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 204 AA; 22685 MM; 009CP65D8B1PBDF2 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA.
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100.0%; Pred. No. 8.2
ive 0; Mismatches
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Lancet 359:1819-1827(2002).
EMBL, AP004205, BAB95171.1; -.
InterPro; IPR000934; AcPasse_VanPerase.
InterPro; IPR000326; PA_PTPasse.
Pfam; PF01569; PAP2; 1.
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InterPro; IPR008934; AcPase_VanPerase.
InterPro; IPR000326; PA_PTPase.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                           Zhang Y., Ren S., Li H., Pu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.;
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016747; AA004706.1; -.
InterPro; IPR008934; Accesse VanPerase.
InterPro; IPR009326; PA_PTPASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSCY...
PSCY...
Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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100.0%; Pred. No. 8.2;
vative 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.2;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF01569; PAP2; 1. -
SMART; SM00014; acidPpc; 1. -
Hypothetical protein; Complete proteome.
SEQUENCE 204 AA; 22838 MW; CC6635270009F674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 22:991-1003(1996).
EMBL; U56077; AAC44782.1; -.
SEQUENCE 206 AA; 23971 MW; 8DDOE751E26BDFA8 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Type III export protein PscK.
PSCK OR PA1724.
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Last annotation update)
                                                                                            Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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MEDLINE=97126825; PubMed=8971719;
                                                   Conserved hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
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nes 8; Conservative
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                                                                                                                                                                                                                    STRAIN-ATCC 12228;
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P95439;
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Matches
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P95439
AC P9543
AC P9543
AC O1-MA
DT 01-MA
DT 0
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091313
1D 09131
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DT 01-MA
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MEDLINE-2043737; PubMed=10984043;

MEDLINE-2043737; PubMed=10984043;

MEDLINE-2043737; PubMed=10984043;

MICKEY M.J., Brinkman R.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Golltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.B.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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100.0%; Pred. No. 8.3;
ative 0; Mismatches
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Best Local Similarity
8; Conserva
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                                                                                                                      SEQUENCE PROM N.A.
                                                               NCBI_TaxID=287;
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Novel Human Human Human Human

Human Human

Ada57610

Novel Human

Ada57611
Aba1270
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Aba1127
Aba1128
Aba1138
Aba1351
Aba166818
Aba66818
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Aba671925
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Aba671925
Aba67114
Aba1825
Aba681236

Human Human Human Human Human Novel

Human

Perfect score:

Sequence:

1

OM protein

on:

Run

Scoring table:

Searched:

88

Minimum | Maximum |

Database

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The present sequence is the murine confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfemily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell.cell interactions and anglogenesis, and in the modulation of wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.
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Pred. No. 1.2e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine confluency regulated adhesion molecule 1.
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            ADA57611
ADA57309
ABD471277
ABD11378
ABD71138
ABD741034
ABD74407
ABD74407
ABD74407
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ABD741407
ABD7407
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(RMFD-) RMF DICTAGENE
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Best Local Similarity
N-PSDB; AAA97189
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Abu80867
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
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AAB80272
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                      PIDSRANPRPONSSPHVNSBYGTLVFNAVHKDDSGQYYCLASNDAGAARCDGQDMBVYDL 240
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                                                                                                                         NDRKEVDEITIBLIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the human confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and anglogenesis, and in the modulation of wound healing
                                                                       SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
                                     MALSERILRIERYARLPHFFLLILFRGCMIBAVNIKSSNRNPVVHBFESVELSCIITHSQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.
                       MALSRRLRLRLYARLPHFPLLLLFRGCMI BAVNLKSSNRNPVVHBFBSVELSCI I THSQT
 Gaps
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Mismatches
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310; Conservative
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          Gaps
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/note= "Casein kinase II phosphorylation site"
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          Indels
 Pred. No. 1.2e-122;
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/note= "N-myristoylation site"
296. .299
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215. .220
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/label= Signal_peptide
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phosphorylation site"
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llarity 100.0%; P:
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Human; immune related disease; diagnosis; antiinflammatory; cardiant;
dermatological; antiarthritic; antirheumatic; immunosuppressive;
haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
antiachmatic; systemic lupus erythematosus; rheumatoid arthritis;
osteoarthritis; spondyloarthropathy; systemic solerosis; arcoidosis;
diopathic inflammatory myopathy; Sjogren's syndrome; thyroidilis;
autoimmune thrombocytopaenia; immune-mediated renal disease;
demyelinating disease; hepatobiliary disease; Mihipple's disease;
inflammatory bowel disease; gluten-sensitive enteropathy;
autoimmune disease; juten-sensitive enteropathy;
mutoimmune disease; transplantation associated disease;
munnological disease; transplantation associated disease;
my graft rejection; graft-versus-host-disease.
                                                                                                              Human PR01868 protein UNQ859 SEQ ID NO:193.
                        AAB33457 standard; protein; 310 AA
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99US-0123618P.
99US-0123957P.
99US-0125775P.
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99US-0132371P.
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99US-0141037P.
99US-0144758P.
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99WO-US020111.
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99US-0162506P.
99WO-US028214.
99WO-US028313.
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18-FEB-2000;
22-FEB-2000;
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                                                       AAB33457;
            AAB33457
RESULT
                             This is PROISED, a putative homologue of A33 antigen, a known colorectal cancer-associated marker. The invention concerns novel secreted and transmembrane proteins, designated PRO polypeptides. The CDNA and gene sequences are useful in the recombinant production of PRO polypeptides, as a hybridization probe to screen libraries to isolate cDNAs with sequence identity to PRO polypeptides or to map the gene encoding the PRO polypeptides and analyzing genetic disorders. The CDNA-gene can also be used to produce transgenic animals useful for the development and screening of therapeutically useful reagents. They can also be used in gene therapy, e.g. to replace a defective gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDRKEVDBITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encodes a PRO polypeptide which is transmembrane polypeptide.
                                                                                                                                                                                                                                                                                 W, Goddard
Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.3%; Score 1409; DB 3; Length 310; Best Local Similarity 85.8%; Pred. No. 1.1e-104; Matches 266; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                 Fong S, Gao
A, Tumas D,
                                                                                                                                                                                                                                                                                 Ferrara N, Fol
, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Pig 14; 154pp; English.
                                                                                  980S-0112851P.
980S-0113118-P.
980S-0113511P.
990S-0115758-P.
990S-011573-P.
990S-0119341P.
990S-0119965-P.
                                                           99WO-US028634
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                                                                                                                                                                                                                                                                                  Desnoyers L,
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                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-431586/37.
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA51265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 310 AA;
 WO200036102-A2
                                                                                                                                             12-JAN-1999;
12-JAN-1999;
09-PEB-1999;
10-PEB-1999;
12-FEB-1999;
                                                         01-DEC-1999;
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                             22-JUN-2000.
                                                                                                   16-DEC-1998;
22-DEC-1998;
                                                                                                                                12-JAN-1999;
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                                                                                                                                                                                                                                                                                                Gurney AL,
Wood WI;
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Human confluency regulated adhesion molecule 1 #2

(first entry)

23-FEB-2001

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic scierosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thromboortopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel diseases, allergic diseases, immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including cariments and hybridisation probes used in the isolation of the numan PRO sequences. AACSBS79 to AACSBS71 t
                                                                                                                                                                                                                                                                                                                                      Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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                                                                                                     Henzel
                                                                                              Gurney AL, Hebert C, He D, Shelton DL, Smith V; Wood WI, Yan M;
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                                                                                                 P, Goddard A,
an J, Pennica D
Watanabe CK, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Fig 88; 309pp; English
                                                                                              Ashkenazi AJ, Baker KP,
Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
                                                                                                                                  Lu Y, Pa
Tumas D,
                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                       WPI; 2000-572271/53.
N-PSDB; AAC58622.
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NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSBEG 300
                                                             SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                                              NDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
                                                                                                            PTDSRANPRPQNSSPHVNSBTGTLVPNAVHKDDSGQYYCIASNDAGAARCEGQDWBVYDL 240
                                                                                                                                                          SDPRIEWKKIQDGQTTYVYPDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
           1 MALRRPPRIALCARLEDFFILLLFRGCLIGAVNIKSSNRTPVVQFFSSVELSCIITDSQT 60
MALSRRLRLRLYARLPHPFLLLLPRGCMIBAVNLKSSNRNPVVHBFBSVBLSCIITHSQT
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AAB27276 standard; protein; 310 AA.

AAB27276

AAB27276;

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180
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                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the human confluency regulated adhesion molecule 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein and coding sequence can be used in the treatment of cancer, inflammation, to modulate cell-cell interactions and anglogenesis, and in the modulation of wound healing
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                                                                                                                                                                                                                                                                                                                                                Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or CRAM-2) polypeptide, useful for treatment of tumors, inflammation reactions and modulating vascular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLOCQESEGYPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PTDSRANPRFQNSSFHVNSRTGTLVFNAVHKDDSGQYYCIASNDAGAARCBGQDMEVYDL
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                                                Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; human; confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 86.3%; Score 1409; DB 3; Local Similarity 85.8%; Pred. No. 1.1e-104; nes 266; Conservative 18; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2, Fig 6; 59pp; English.
                                                                                                                                                                                             13-MAR-2000; 2000WO-EP002219.
                                                                                                                                                                                                                       99BP-00200746
                                                                                                                                                                                                                                                                               Imhof BA, Aurrand-Lions M;
                                                                                                                                                                                                                                                   (RMFD-) RMP DICTAGENE SA
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                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA95306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310 AA;
                                                                                                                                       WO200053749-A2
                                                                                                                                                                                                                         11-MAR-1999;
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ID AABB
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The present sequence is one of sixty one novel secreted and transmembrane diseases (e.g. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung aquamous cell carcinoma), gastrointestinal disorders (e.g. entercoolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosolerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), inflammatory infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                       antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.
                                                                                             dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty one nucleic acids encoding PRO polypeptides which are useful treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squ cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ, Botstein D, Desnoyers L, Pilvaroff E, Pong S, Gao W, Gerber H Godowski PJ, Grimaldi CJ, Gurney AL, Paoni NF, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 124; 393pp; English
                                                                                                                                                                                                                                                                                               22-PEB-2000; 2000WO-US004414
                              24-APR-2001 (first entry)
                                                           Human PRO1868 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                   WO200104311-A1
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29-NOV-1999;
30-NOV-1999;
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13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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AAB80272;
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99US-0143048P. 99US-0145698P. 99US-0146222P. 99WO-US020594.

99WO-US021090. 99WO-US021547.

99WO-US023089 99WO-US028214 99WO-US028313 99WO-US028564 99WO-US028565 99WO-US030095 99WO-US030911 99WO-US030999 2000WO-US000219

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length
                                                                                                                                                                                           180
                                                                                            SDPRIBWKKIQDGQTTYVYPDNKIQGDLAGRIDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
                                                                                                             61 SDPRIEWKKIQDEQTYTVPFDNKIQGDLAGRAEILGKYSLKIWNVTRRDSALYRCEVVAR 120
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                                                 1 MALER P PRILICAR L POPPLILIZA PROCLIGAVNIKS SNRTPVVQEPESVELSCIITDSQT
                                                                                                                                                                              241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDBEG
                                                                                                                                                                                                                                              181 PTDSRANPRFRNSSPBLANSTGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMBVYDL
                              1 MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHBFESVELSCIITHSQT
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a T, Nagai K, Kojima S, Otsuki T, Koga
ö
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Indels
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26;
18; Mismatches
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11-JAN-2000; 2000JP-00118774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
266; Conservative
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Wakamatsu A, Sugiyama
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N-PSDB; AAK94867.
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 Matches
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Length 310;

Score 1409; DB 4; Pred. No. 1.1e-104;

86.3%;

Query Match Best Local Similarity

ME, Goddard A; Kljavin IJ; Tumae D;

Desnoyers L, Baton DL, W, Gerber H, Gerritsen Gurney AL, Hillan KJ, F, Roy MA, Stewart TA,

Wood WI:

Ferrara N;

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99WO-US028551.
99WO-US028551.
99WO-US028564.
99WO-US028565.
99US-01702628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US028301
                                                                                                                       Query Match 86.3%
Best Local Similarity 85.8%
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                DFRHKSSFVI 310
                                                                                                       Sequence 310 AA;
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01-DBC-1999;
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human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from BPO
                                                                                                 1 MALRRPPRIRICARLPDFFLLILFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT
                                                                                                                                                                                             PIDSRANPRFONSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL
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                                                                      Gaps
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T, Koga
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                                                     Length 310;
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                                                                    26; Indels
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping
                                                   Query Match
Best Local Similarity 85.8%; Pred. No. 1.1e-104;
Matches 266; Conservative 18; Mismatches 26;
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K, Kojima
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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N-PSDB; AAK94243.
                                   Sequence 310 AA;
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clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Frimers for synthesising the full length cDNA molecules have for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from RPO
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85.8%; Pred. No. 1.1e-104;
tive 18; Mismatches 26;
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Deforge L, Desnoyers L, Filvaroff B, G
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                        2000WO-US005601.
2000WO-US005841.
2000US-0187202P.
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2000WO-US023522.
2000WO-US023328.
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2000WO-US005004.
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2000WO-US014042.
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02-JUN-2000; 2000WO-US015264.
                99WO-US031243
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                                 2000MO-US000219
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2000WO-US000376
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99WO-US030911
99WO-US030999
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                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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N-PSDB; AAS21512.
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                                      06-JAN-2000;
06-JAN-2000;
11-PEB-2000;
18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
                                                                                                                               10-MAR-2000;
15-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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02-MAR-2000;
03-MAR-2000;
                       30-DEC-1999;
05-JAN-2000;
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24-PBB-2000;
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                                                                                                                                                                                                                                                                                                        Smith V,
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ANU12172-AAU12446 represent novel human secretory and transmembrane FRO polypeptides. The FRO polypeptides are useful to detect other FRO polypeptides. To link bioactive molecules to cells expressing FRO polypeptides, to link bioactive molecules to cells expressing FRO polypeptides, to modulate biological activities of cells expressing FRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing FRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TWP-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or agene expression in pericyte cells, the release of prolecoglycans from cartiage, the proliferation of inner ear utricular supporting cells or of T-proliferation of inner ear utricular supporting cells or of T-proliferation of inner ear utricular supporting cells or of T-propreptides may modulate glucose or free faity acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor collypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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preparations
    DB 4; Length 310;
    86.3%; Score 1409;
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Sequence 310 AA;

Query Match

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                                                                                                               61 SDPRIEWKKIQDEGTTYVPFDIKIQGDLAGRAERILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, serebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.
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                                                                                                61 SDPRIEWRKIQDGQTTYVYPDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCEVVAL
                                                           1 MALRRPPRIRICARLPDPFILILPRGCLIGAVNLKSSNRTPVVQBFESVBLSCIITDSQT
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                                         1 MALSRRIRIRLYARLPHPPLILLFRCCMIBAVMLKSSNRNPVVHBPBSVBLSCIITHSQT
              Gaps
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Komatsoulis GA;
             Indels
Pred. No. 1.1e-104;
8: Mismatches 26;
              18; Mismatches
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Birse CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein encoded by gene #13
                                                                                                                                                                                                                                                                                                                                                                                                                                AABB0383 standard; protein; 310 AA.
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Olsen HS,
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85.8%;
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                266; Conservative
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Shi Y, Lafleur DW,
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 Local Similarity
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disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
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Komatsoulis (
                                                                                           86.3%; Score 1409; DB 4;
85.8%; Pred. No. 1.1e-104;
iive 18; Mismatches 26;
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Birse CE,
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Olsen HS,
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Best Local Similarity
Matches 266; Conserv
                                                                      Sequence 310 AA;
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                                           preparations
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Shi Y, Lai
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                                                                                                                                                                   NIAGIIGGVLVVLIVLAVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTSREG 300
                                                                                                                                                      SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
                                                                                                                                                                                                           NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQBSEGYPRPHYSWYRNDVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding 29 secreted proteins, for diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA;
                                                                                                             PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL
                                                                                                                                                                                                                                                                                MALSRRIRLRLYARLPHPFLLLLFRGCMIBAVNLKSSNRNPVVHBPBSVBLSCIITHSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to 29 human secreted proteins. The
                                                                      ö
                                           Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ni J, Soppet DR,
Komatsoulis GA;
                                                                    26; Indels
                                         86.3%; Score 1409; DB 4;
85.8%; Pred. No. 1.1e-104;
iive 18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duan RD, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 557-558; 601pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein encoded by gene #38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB80408 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebner R,
Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2000; 2000WO-US019735.
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                                   Query Match
Best Local Similarity 85.8%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                               DPRHKSSPVI
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                 Sequence 310 AA;
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Shi Y, La
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SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
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The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
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                                                                                                                                                                                                                         1 MALRRPPRIRICARLPDFFLLILFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSOT
                                                                                                                                                                                                                                                                                                                       NDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQBSEGYPRPHYSWYRNDVPL
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                                                                                                                                                                                                            MALSRRIRLRLYARLPHFFLLLLFRGCMI RAVNLKSSNRNPVVHEFESVELSCI I THSQT
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, secreted and transmembrane protein, PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434, PRO1927, inflammatory disorder, immune related disease, rheumatoid arthritis.
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                                                                                                                                                     Length 310;
                                                                                                                                                                                 26; Indels
                                                                                                                                                    ; Score 1409; DB 4;
; Pred. No. 1.1e-104;
18; Mismatches 26;
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980S-0113145P.
980S-0113511P.
990S-0115558P.
990S-011553P.
                                                                                                                                                     86.3%;
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                                                                                                                                                                                 Matches 266; Conservative
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                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                           Sequence 310 AA;
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                                                                                               preparations
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12-JAN-1999;
12-JAN-1999;
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The inversion transce to an instance puryperce marking or transcendent amino acid sequence identity to secreted and transmembrane polypeptides PRO1800, PRO539, PRO982, PRO1844, PRO1863, Also included are vectors, host cells and antibodies against PRO polypeptides. PRO1868 useful for the diagnosis and treatment of inflammatory and immune related diseases including systemic lupus erythematosis, rheumatoid arthritis, systemic contructions hepatitis, psoriasis, allergic diseases of the lung and graft-cerosis, autoimmune hemolytic anaemia, thyroiditis, diabetes mellitus, infectious hepatitis, psoriasis, allergic diseases of the lung and graft-cerosis, autoimmune hemolytic anaemia, thyroiditis, diabetes mellitus, infectious hepatitis, psoriasis, allergic diseases of the lung and graft-constructing hybridisation probes for mapping the gene that encodes that the genetic analysis of individuals with genetic disorders, and for generating transgenic animals which are useful in the development can servening of therapeutically useful reagents. PRO nucleic acids are electrophoresis purposes. The anti-PRO antibodies are useful in case are electrophoresis purposes. The anti-PRO antibodies are useful in genetic calls, tissues or serum and for affinity purification of PRO. The present sequence represents a PRO protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel secreted and transmembrane polypeptides and polynucleotides useful for diagnosis and treatment of inflammatory disorders and immune-related diseases, and identifying modulators.
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Watanabe CK;
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, Stewart TA,
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09-FEB-1999; 99US-0119341P.
10-FEB-1999; 99US-0119537P.
12-FEB-1999; 99US-0119965P.
02-JUN-1999; 99US-0119965P.
29-OCT-1999; 99WG-US012252.
03-DEC-1999; 99WG-US028653.
03-DEC-1999; 99WG-US028653.
03-DEC-1999; 99WG-US028651.
03-DEC-1999; 99WG-US028651.
03-PEB-2000; 2000WG-US003865.
22-FEB-2000; 2000WG-US008419.
03-MAR-2000; 2000WG-US008419.
30-MAR-2000; 2000WG-US008419.
30-MAR-2000; 2000WG-US014941.
03-MAR-2000; 2000WG-US014941.
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Pan J, Roy MA,
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N-PSDB; ABS68392.
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Wood WI;
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                        Human; secreted protein; transmembrane protein; gene mapping; transgenic;
      PTDSRAN PRPQNSSPHVNSETGTLV PNAVHKDDSGQYYCIASNDAGAARCEGQDMBVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted and transmembrane (PRO) polypeptides, useful for treating conditions requiring PRO polypeptides, for screening PRO antagonists and agonists useful as drug candidates.
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Watanabe CK;
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D,
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                                                                                                ABG91361 standard; protein; 310 AA.
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                                                                                                                                       Novel human secreted protein #7.
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9805-0113115P
9805-0113511P
9905-0115558P
9905-0115731P
9905-011931P
9905-011931P
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2000MO-US014941.
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                                                                                                                                                                                                             2001US-00033246
                                                                                                                          (first entry)
                                                   DFRHKSSFVI 310
                                                            DFRHKSSFVI 310
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                                                                                                                                                                                    US2002098505-A1.
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11-FEB-2000;
22-FEB-2000;
02-MAR-2000;
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12-JAN-1999;
12-JAN-1999;
12-JAN-1999;
09-FEB-1999;
10-FEB-1999;
02-JUN-1999;
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30-MAR-2000;
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                                                                                                                          29-NOV-2002
                                                                                                                                                                                                                                                                                                               DEC-1999;
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                                                                                                                                                            immunogenic.
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01-DEC-1999
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Wood WI;
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to new human secreted and transmembrane proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NDRKEVDRITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQRSEGYPRPHYSWYRNDVPL
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Matches 266; Conservative
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          invention relates
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2000WO-US030952.
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20-JUN-2001; 2001WO-US019692
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01-MAR-2001;
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## (GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NP, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

## WPI; 2002-090516/12. N-PSDB; ABL88202.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

# Claim 11; Pig 262; 565pp; English.

ABBBS003. The PRO proteins and polymucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angions, myccardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene exemplification of the present invention ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

### Sequence 310 AA;

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 Length 310;
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86.3%; Score 1409; DB 5;
85.8%; Pred. No. 1.1e-104;
ive 18; Mismatches 26;
Query Match 86.3
Best Local Similarity 85.8
Matches 266; Conservative
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APPLICANT: Geritteen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Renneth, J.
APPLICANT: Hillan, Renneth, J.
APPLICANT: Hallan, Renneth, J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thans, P. Mickey
APPLICANT: Thans, P. Mickey
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APPLICANT: Williams, P. Mickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 423, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
  Sherman
     Fong,
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### PRPLICANT: Williams, p. Hickey
### PRPLICANT: Word, williams, p. Hickey
### PRPLICANT: Word, williams, p. Hickey
#### PRPLICANTON WINGER: US/09/905,125A
### CORRENT OF TILNG DATE: 2010-02-22
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### PRIOR PLILING DATE: 1999-07-07
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85.8%; Pred. No. 1.1e-133;
tive 18; Mismatches 26; Indels
Grimaldi, Christopher J.
                                   Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
                                                                                                                                                                     Pan, James
Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                 rumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Homo Sapien
US-09-905-125A-423
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NDRKGVDEITIELIVQVXPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTDSRANPRFONSSFHVNSBTGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240
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85.8%; Pred. No. 1.1e-133;
ive 18; Mismatches 26; Indele
              FRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-05
PRIOR PLILING DATE: 1999-12-05
PRIOR PLILING DATE: 1999-12-05
PRIOR PLILING DATE: 1999-12-20
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Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botteein, David
APPLICANT: Botteein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Blen
APPLICANT: Fivaroff, Blen
APPLICANT: Fivaroff, Blen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.3 Best Local Similarity 85.8 Matches 266; Conservative
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ORGANISM: Homo Sapien
US-09-907-794A-423
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SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDPRIEWKKIQDEQTTYVPFDNKIQGELAGRABILGKTSLKIWNVTRRDSALYRCEVVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 310;
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86.3%; Score 1409; DB 4;
Best Local Similarity 85.8%; Pred. No. 1.1e-133;
Matches 266; Conservative 18; Mismatches 26;
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TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PEOSO3P.108
FULLE OF INVENTION NUMBER: US/09/152,060
CURRENT PILING DATE: 1998-09-11
EARLIER PPLICATION NUMBER: PCT/US98/04858
EARLIER PILING DATE: 1999-03-14
EARLIER PILING DATE: 1997-03-14
EARLIER PILING DATE: 1997-05-30
EARLIER PPLICATION NUMBER: 60/048,100
EARLIER PPLICATION NUMBER: 60/048,100
EARLIER PILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF ESQ ID NOS: 423
SEQ ID NO 423
LENGTH: 310
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FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/048,970
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CORGANISM: Homo Sapien
US-09-902-775A-423
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EARLIER I
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR PPLION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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PILING DATE: 1999-09-15
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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PLING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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US-09-902-775A-423
Sequence 423, Application US/09902775A
; Patent No. 6686451
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Bllen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanapeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
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Katon, Dan L.
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APPLICANT:
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Mather, Jennie P.
Pan, James
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Hillan, Kenneth,
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Eaton, Dan L.
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                                                                                         ORGANISM: Homo sapiens
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PRIOR PILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 9
LENGTH: 312
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                                                                                                            US-09-254-465A-9
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APPLICANT:
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austrin L.
APPLICANT: Gurney, Austrin L.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OP DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OP DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OP DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
TITLE OF INVENTION: OP DISEASES
CURRENT FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-11-20
FRIOR PILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: US 60/066,364
FRIOR APPLICATION NUMBER: PCT/US98/19437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLOCQESEGYPRPHYSWY 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MARRSEHRI-------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVXYQBAILAC-K 51
                                                                                                                                                                                                                                                                                                                                                                                                                           3 LSRRIRLRIYARLPHFFLLLLFRGCMI -----EAVNLKSSNRNPVVH--EFESVELSCII 55
                                                                                                                                                                                                                                                                                                                                                                                          26; Gaps
                                                                                                                                                                                                                                                                                                                                                  30.5%; Score 498; DB 4; Length 298; 37.0%; Pred. No. 6.2e-42; ive 61; Mismatches 112; Indels
                 EARLIER APPLICATION NUMBER: 60/668,368
EARLIER PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 298
TYPE: PRT
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Patent No. 6410708
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     EARLIER FILING DATE: 1997-06-06
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Ashkenazi, Avi J.
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Best Local Similarity 37.09
Matches 117; Conservative
                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                      NAME/KEY: SITE
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116 EVVALNDR-KEVDRITIBLIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
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                                                                                                                                                                                                                                175 RNDVPLPTDSRANPRFQNSSFHVNSBTGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQD 234
                                                                                                 3 LSRRLRLRLYARLPHFFLLLLFRGCMI-----EAVNLKSSNRNPVVH--BFBSVELSCII 55
                                                                                                                                      1 MARRISRHRL--------LILLILRYLVVALGYHKAYGFSAPKDQQVVTAVEYQRAILAC-K 51
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                                                  22; Gaps
Query Match 29.3%; Score 478; DB 4; Length 31 Best Local Similarity 36.3%; Pred. No. 6.9e-40; Matches 110; Conservative 62; Mismatches 109; Indels
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TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J.
Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
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Pilvaroff, Ellen
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APPLICANT: MILIDIANA; F. MILICRAY; ADDILICANY: MILIDIANA; I. MILICAY; APPLICANT: MILIDIANA; I. MILICAY; APPLICANTION: Secreted and Transmembrane Polypeptides and Nucleic TITIES OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITIES OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITIES OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR APPLICATION NUMBER: POLO-07-12
PRIOR PILING DATE: 1999-07-05 (0/14,048)
PRIOR FILING DATE: 1999-07-05 (0/14,022)
PRIOR PAPLICATION NUMBER: US 60/146,222
PRIOR PAPLICATION NUMBER: US 60/146,222
PRIOR PAPLICATION NUMBER: PT/US99/20594
PRIOR FILING DATE: 1999-07-05 (0/14,022)
PRIOR PAPLICATION NUMBER: PT/US99/20594
PRIOR APPLICATION NUMBER: PT/US99/20594
PRIOR PRILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PT/US99/20594
PRIOR APPLICATION NUMBE
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Grimaldi, Christopher J.
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Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT:
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62; Mismatches 109;
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILIGA DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-8
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-0.0
PRIOR PILING DATE: 1999-12-0.0
PRIOR PILING DATE: 1999-12-0.0
PRIOR PILING DATE: 1999-12-10
PRIOR PILING DATE: 1999-12-10
PRIOR PILING DATE: 1999-12-20
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ORGANISM: Homo sapiens
US-09-907-794A-64
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29.3%; Score 478; DB 4; Length 312;

Query Match

Sequence 64, Application US/09905125A Patent No. 6664376

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                                                                                                                                       EVVALNDR-KEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWY 174
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                                                                                                                                                                                                                                                                                                                     MEVYDLNIAGIIGGVLVVLIVLAVITMGICCAYRRGCF---ISSKQDGESYKSPGKHDGV 291
                                                  3 LSRRLRLYARLPHPFLLLLFRGCMI-----RAVNLKSSNRNPVVH--EFBSVELSCII 55
                                                                        1 MARRSRHRL-------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC-K 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
36.3%; Pred. No. 6.9e-40;
tive 62; Mismatches 109; Indels
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary B.
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Paoni, Nicholas P.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Best Local Similarity 36.3
Matches 110; Conservative
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US-09-902-775A-64
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56 THSQTSDPRIEWKKIQDGQTTYVYPDNKIQGDLAGRIDVPGKTSLRIWNVTRSDSAIYRC 115
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                                                              PRIOR FILLY NAMER: PCT/US99/21547
PRIOR PLING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
                                                                                                                                                                                                                                                                                                                                          FRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 64
LENGTH: 312
TYPE: PRI
                    APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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Patent No. 6410708
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Ashkenazi, Avi J.
Fong, Sherman
Goddard, Audrey
Gurney, Austin L.
Napier, Mary A.
1999-09-13
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Wood, William I
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US-09-902-775A-64
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15 PILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72
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US-09-462-270-2
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TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
CURRENT APPLICATION NUMBER: US/09/254,465A
CURRENT FILING DATE: 1999-03-05
FRIOR APPLICATION NUMBER: US/09/254,465A
FRIOR PILING DATE: 1998-11-20
FRIOR PILING DATE: 1998-11-20
FRIOR PILING DATE: 1997-11-21
FRIOR APPLICATION NUMBER: US 60/066,364
FRIOR PILING DATE: 1998-03-20
FRIOR PILING DATE: 1998-03-20
FRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NOS: 30
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Sequence 313, Application US/09188930A
Sexustal INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Lorna Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT PAPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SEQ ID NOS: 348
SEQ ID NO 331
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ORGANISM: Mus musculus
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US-09-188-930-331
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18 FFLLLLFRGCMIEAVNLKSSNRNPVVHBFESVELSCIITHSQTSDPRIEWKKIQDGQTTY

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137
                            138 KPVTPVCRIPAAVPVGKTATLQCQESBGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHV 197
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78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKBVDEITIBLIVQV
                                                                                                                                                                                                                                                                                              257 AVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
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Sequence 2, Application US/09462270;
Batent No. 635870;
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
ITILE OF INVENTION: Receptor Involved in Platelet Aggregation;
ITILE OF INVENTION: Receptor Involved in Platelet Aggregation;
ITILE OF INVENTION: Receptor Involved in Platelet Aggregation;
CURRENT APPLICATION NUMBER: US/09/462,270
CURRENT PILING DATE: 1997-07-10
RIGHER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 299
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Ashkenazi, Avi
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ORGANISM: HOMO SAPIENS
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APPLICANT:
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TYPE: PRT
ORGANISM: Mouse
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       US-09-312-283C-189
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US-09-312-283C-331
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APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT
TITLE OF INVENTION: OP DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
FILE REFREENCE: P1216R1 (US)
FILE REFREENCE: 1999-03-05
FRIOR FILING DATE: 1999-13-05
FRIOR PRILING DATE: 1999-11-21
FRIOR PRILING DATE: 1999-11-21
FRIOR PRILING DATE: 1999-03-06
FRIOR PRILING DATE: 1999-03-06
FRIOR FILING DATE: 1999-03-07
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25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels
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Sequence 189, Application US/09312283C
Sequence 180, Separation US/09312283C
GENERAL INFORMATION:
APPLICANT: Witson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: and Methods for Their Use
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CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 299
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ORGANISM: Homo sapiens
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ORGANISM: Mouse
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                                                                                                                    15 PILATILCSLALGSVIVHSSEBEVRIPENNPVKLSC--AYSGFSSPRVEWKFDQGDTTRL 72
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Sequence 331, Application US/09312283C

GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Muxison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REPERBNCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
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33.8%; Pred. No. 1.4e-33;
tive 50; Mismatches 132; Indels
Query Match
25.4%; Score 415; DB 4; Length 299;
Best Local Similarity 33.8%; Pred. No. 1.4e-33;
Matches 100; Conservative 50; Mismatches 132; Indels
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Best Local Similarity 33.8%
Matches 100; Conservative
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SEQ ID NO 119
LENGTH: 299
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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
   GILVFGIWFAYSRGHFDRTKKGTSSKK-----VIYSQPSARSEGEFKQTSSFLV 299
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CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT PILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-11-39
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-39
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-11-39
PRIOR PILING DATE: 1999-11-39
PRIOR PILING DATE: 1999-11-39
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28654
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
                                                                                          RESULT 15
8-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 6635468
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT:
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'(gm2_6')ptodata'/I)pupaa/USO7_NEW_PUB.ppp:*

'(gm2_6')ptodata'/I)pupaa/USO6_NEW_PUB.ppp:*

'(gm2_6')ptodata'/I)pupaa/USO6_PUBCOMB.ppp:*

'(gm2_6')ptodata'/I)pupaa/USO7_NEW_PUB.ppp:*

'(gm2_6')ptodata'/I)pupaa/USO8_NEW_PUB.ppp:*

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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                   OM protein - protein search, using sw model
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB
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APPLICANT: Mood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR APPLICATION NUMBER: US 60/143,048 Sequence 423, Sequence 423, Sequence 423, Sequence 423, Sequence s US-09-909-1320-423 US-09-905-291A-423 US-09-905-291A-423 US-09-907-824-423 US-09-907-841-423 US-09-907-841-423 US-09-906-742-423 US-09-906-742-423 US-09-906-742-423 US-09-907-613-423 US-09-907-613-423 US-09-907-613-423 US-09-904-859-423 US-09-904-859-423 US-09-904-829-423 US-09-904-820-423 

Sequence Sequence Sequence Sequence

Sequence A

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Sequence 423, App	
US-09-906-646-423 US-09-906-700-423 US-09-903-786-423 US-09-903-749A-423 US-09-904-119-423 US-09-904-119-423 US-09-904-119-423 US-09-904-423-423 US-09-907-925-423 US-09-907-925-423 US-09-907-925-423 US-09-907-925-423 US-09-907-925-423 US-09-907-925-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-644-423 US-09-905-615-423 US-09-905-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423 US-09-907-615-423	ALIGNMENTS 009320 LET J.
	on US/09999 (0A1 Inc. Avi David Lac Inc. Avi Sapoleone Blen man Inglang unspeter Mary E. V.
	aation US/095 32240A1 ih, Inc. azi, Avi ih, David ars, Luc Dan L. a, Napoleone Af, Blen Sherman il-Qiang Hangpetar Hangpetar Sherman Anagrit A.
	SULT 1  -09-90-320-423  Sequence 423, Application US/09909320  Bequence 423, Application US/09909320  GENERAL INFORMATION:  APPLICANT: Genetech, Inc.  APPLICANT: Bettein, David  APPLICANT: General Napoleome  APPLICANT: Follow, Sherman  APPLICANT: Geriber, Hanspeter  APPLICANT: Geriber, Hanspeter  APPLICANT: Geriber, Paul J.  APPLICANT: Godowski, Paul J.  APPLICANT: Grandid, Christopher J.  APPLICANT: Grandid, Christopher J.  APPLICANT: Grandid, Christopher J.  APPLICANT: Grandid, Christopher J.  APPLICANT: Mather, Jemneth, J.  APPLICANT: Mather, Jemneth J.  APPLICANT: Roy, Margaret Ann  APPLICANT: Roy, Margaret Ann  APPLICANT: Timothy A.  APPLICANT: Timothy A.  APPLICANT: Timas, Daniel
1 1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	9-320- No. 10 No
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APPLICANT: Paoni, Names
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION Acids Encoding the Same
TITLE OF INVENTION ACIDS (19/99)90,088B
CURRENT APPLICATION WHERE: 1046-1141
PRIOR APPLICATION WHERE: US 60/143,048
PRIOR APPLICATION WHERE: 05 60/145,698
PRIOR APPLICATION WHERE: 05 60/146,222
PRIOR APLING DATE: 1999-00-26
PRIOR APLING DATE: 1999-00-15
PRIOR APLING DATE: 1999-00-15
PRIOR APLICATION WHERE: PT/WS99/2094
PRIOR APLICATION WHERE: PT/WS99/2094
PRIOR APPLICATION WHERE: PT/WS99/2091
PRIOR APPLICATION WHERE: PT/WS99/
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Kljavin, Ivar J.
Mather, Jennie P.
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Hillan, Kenneth,
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Best Local Similarity 85.8
Matches 266; Conservative
                                                                                                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Homo Sapien
US-09-909-088B-423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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86.3%; Score 1409; DB 9;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26;
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
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; Patent No. US20020146709A1
; GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPRHKSSFVI 310
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ORGANISM: Homo Sapien
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Bestein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Blen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
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85.8%;
APPLICATION NUMBER: PCT
FILING DATE: 1999-09-15
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Best Local Similarity 85.8<sup>†</sup>
Matches 266; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423
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CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembra:
TITLE OF INVENTION: Acids Encoding the Same
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Sequence 423, Application US/09905291A
Setent No. US20020160374A1
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
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Eaton, Dan L.
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61 SDPRIEWKKIODGOTTYVYFDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSALYRCEVVAL 120
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8; Pred. No. 3.6e-118;
18; Mismatches 26;
PRIOR FILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-10-05
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PRIOR PILLING DATE: 1999-12-16
PRIOR PILLING DATE: 1999-12-16
PRIOR PILLING DATE: 1999-12-20
PRIOR PILLING DATE: 2000-01-05
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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Filvaroff, Bllen
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Roy, Margaret Ann
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, Daniel
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D.
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: 1046-61.
FILE REFERENCE: 1046-61.
FILE REFERENCE: 1046-61.
FILO APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 1090-07-10.
FILOR APPLICATION NUMBER: US/09/655,350
FILOR APPLICATION NUMBER: US/01-10-10.
FRIOR APPLICATION NUMBER: US/01-10-10.
FRIOR APPLICATION NUMBER: US/01-22
FRIOR FILING DATE: 1999-07-28
FRIOR APPLICATION NUMBER: US/01-20-24
FRIOR FILING DATE: 1999-09-13
FRIOR APPLICATION NUMBER: PCT/US99/20594
FRIOR FILING DATE: 1999-09-15
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR FLING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR PELING DATE: 1999-11-20
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1990-11-30
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larity 85.8%; Pred. No. 3.6e-118;
Conservative 18; Mismatches 26;
                                             Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                             Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas P.
                                                                                                                                                                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                               Gurney, Austin L.
Hillan, Kenneth, J.
rritgen, Mary E.
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US-09-902-853-423
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Best Local Similarity
Matches 266; Conserv
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wolliam, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US FCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-01
PRIOR PLING DATE: 1999-09-01
PRIOR PLING DATE: 1999-09-15
PRIOR PRIOR PLING DATE: 1999-09-15
PRIOR PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSBEG 300
                                                                                                                                                                                                                                                                                          PTDSRANPRPQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMBVYDL
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FILING DATE: 1999-09-15
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: Pagoni, Nacionas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: NUMBER: US/09/907, 841
CURRENT APPLICATION NUMBER: US 60/143, 048
PRIOR PELING DATE: 1000-00-22
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR APPLICATION NUMBER: PCT/US99/2059
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-10-16
PRIOR PELING DATE: 1999-11-29
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US-09-904-011-423
; Sequence 423, Application US/09904011
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US-09-907-841-423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDPRIBWKKIQDEQTTYVFFDNKIQGDLAGRABILGKTSLKIWNYTRDSALYRCEVVAR 120
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86.3%; Score 1409; DB 9; Length 310;
Best Local Similarity 85.8%; Pred. No. 3.6e-118;
Matches 266; Conservative 18; Mismatches 26; Indels
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-07
PRIOR PPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Desteain, David
APPLICANT: Batcoh, David
APPLICANT: Baton, David
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Geritsen, Mary E.
Goddard, A.
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ORGANISM: Homo Sapien
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LENGTH: 310
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT PILING DATE: 2001-07-16
PRIOR PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
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                                                                                                                                       1 MALSRRIRLRIYARIPHPFILLIFRGCMIRAVNLKSSNRNPVVHBFESVELSCITHSQT
                                                                                            Gaps
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                                              Length 310;
                                                                                            IndelB
                                           86.3%; Score 1409; DB 10;
85.8%; Pred. No. 3.6e-118;
ive 18; Mismatches 26;
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Publication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Pilvaroff, Ellen
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Hillan, Kenneth, J.
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Mather, Jennie P.
                                              Query Match 86.3%
Best Local Similarity 85.8%
Matches 266; Conservative
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Botstein, David
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US-09-904-011-423
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, William: I.
TITLE OF INVENTUON: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTUON: Acids Encoding the Same
FILE REPRENCE: 10466-418
FILE REPRENCE: 10466-418
FILE APPLICATION NUMBER: US/09/904.011
FRIOR APPLICATION NUMBER: O9/665.300
FRIOR APPLICATION NUMBER: PC/1800/0441
FRIOR APPLICATION NUMBER: US/0143.048
FRIOR PILING DATE: 1999-07-22
FRIOR APPLICATION NUMBER: US/0145.698
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-18
FRIOR PILING DATE: 1999-09-15
FRIOR APPLICATION NUMBER: PC/18099/20594
FRIOR PILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-11-20
FRIOR FILING DATE: 1990-11-20
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
  Publication No. US20030003530A1
                                                                                                                                                                                                                                                                  Gerber, Hanspeter
Gerritsen, Mary E
                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
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ORGANISM: Homo Sapien
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Wood, Stewart and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
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85.8%; Pred. No. 3.6e-118;
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CURRENT PEDLICATION NUMBER: US/99906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-13-03
PRIOR PILING DATE: 1999-13-03
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PRIOR PILING DATE: 199
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                               Pong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
                              Perrara, Napoleone
Pilvaroff, Ellen
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Best Local Similarity 85.8
Matches 266; Conservative
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ORGANISM: Homo Sapien
US-09-906-838-423
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APPLICANT:
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                   PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
CATION NUMBER: US 60/146,222
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Publication No. US20030027143A1
GRNERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-00-16
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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APPLICANT: Genencech, Inc.; APPLICANT: Ashkenazi, Avi; APPLICANT: Bestein, David; APPLICANT: Bestoyers, Luc; APPLICANT: Eaton, Dan L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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ORGANISM: Homo Sapien
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT PLLICATION NUMBER: US/09/907,613
CURRENT PLLING DATE: 2000-02-22
FRIOR PTLING DATE: 2000-02-22
FRIOR PLLING DATE: 1999-07-07
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR PLILING DATE: 1999-07-07
FRIOR PLLING DATE: 1999-07-08
FRIOR PLLING DATE: 1999-07-28
FRIOR PLLING DATE: 1999-07-28
FRIOR PLLING DATE: 1999-09-08
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                                                                                                                 SDPRIEWRKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                                                                                                                           121 NDRKEVDBITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180
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                         1 MALRRPPRIRICARLPDPFLLILIFRGCLIGAVNLKSSNRTPVVQRFESVELSCIITDSQT 60
  MALSRRLRLRLYARLPHFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITHSQT
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas P.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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    DB 10;
10; Similarity 85.8%; Pred. No. 3.6e-118; 56; Conservative 18; Mismatches 26;
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121 NDRKEVDEITIELIVQVKEVTEVC. 1PAAVPVGKTATLQCQESEGYPRPHYSHYSHY 180
121 NDRKEIDEIVIELTVQVKPVTEVC:VPKAVPVGKMATLHCQESEGHPRPHYSHYSHYDVPL 180
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
                                                                                                        181 PTDSRANPRFQNSSFHVNSBTGTL/FNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL
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PRIOR FILING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665.350
PRIOR PLING DATE: 2000-02-25
PRIOR PLING DATE: 1090-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-38
PRIOR PLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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Publication No. US20030036060A1
GENERAL INFORMATION:
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
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APPLICANT: Ashkenzi, Avi
APPLICANT: Bottein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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;; Pred. No. 3.6e-118;
18; Mismatches 26;
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                                                        Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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85.8%;
          Gerritsen, Mary E.
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Best Local Similarity
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SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCEVVAL 120
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT FILING DATE: 2001-07-18
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larity 85.8%; Pred. No. 3.6e-118;
Conservative 18; Mismatches 26;
                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-18
PRIOR PRICATION NUMBER: PCT/USOU/04414
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
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PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
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US-09-909-204-423
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; Pred. No. 3.6e-118;
18; Mismatches 26; Indels
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
PRIOR PLING DATE: 1999-12-0
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PRIOR PLING DATE: 1009-12-05
PRIOR PLING DATE: 1000-10-05
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Grimaldi, Christopher J.
Gurney, Autein L.
Hillan, Kenneth, J.
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; Publication No. US20030036061A1
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
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85.8%;
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APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Beston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Bllen
APPLICANT: Fong, Sherman
APPLICANT: Gac, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Grimaldi, Christop
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 266; Conserv
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PRIOR APPLICATION NUMBER: c.,,---
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Williams, P. Mickey
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gerritsen, Mary B.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                              US-09-904-820-423
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CURRENT APPLICATION NUMBER: US/09/04,820

CURRENT FILING DATE: 2001-07-13

PRIOR PILING DATE: 2000-09-18

PRIOR PLILNG DATE: 2000-00-22

PRIOR PLILNG DATE: 2000-02-22

PRIOR PLILNG DATE: 1990-07-26

PRIOR PLILNG DATE: 1990-07-28

PRIOR PLILNG DATE: 1990-07-28

PRIOR PLILNG DATE: 1990-07-28

PRIOR PLILNG DATE: 1990-07-28

PRIOR PLILNG DATE: 1990-07-38

PRIOR PLILNG DATE: 1990-09-13

PRIOR PLILNG DATE: 1990-09-12

PRIOR PLILNG DATE: 1990-10-05

PRIOR PLILNG DATE: 1990-11-20

PRIOR PLILNG DATE: 1990-11-20
                                Sequence 423, Application US/09904820
Publication No. US20030036094A1
GENERAL INPORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Panni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William, I.
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Filvaroff, Bllen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Acids Encoding the Same PILE REPERRUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,786

CURRENT PILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR PILING DATE: 2000-09-18

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 423

SEQ ID NO 423
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Wood, William, I.
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ORGANISM: Homo Sapien
US-09-904-786-423
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OM protein - protein search, using sw model

June 15, 2004, 10:59:09; Search time 14.5 Seconds (without alignments) 2056.508 Million cell updates/sec Run on:

US-09-524-531C-13

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Score	415	181	180	178	177	172.5	169.5	169.5	169	169	167.5	167.5	166	164.5	164.5	164	163	162	162	160	159.5	158.5	157	156	156	156	154.5	153.5	153
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#### ALIGNMENTS

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CiDate: 2	CiDate: 27-Oct-1995 #sequence revision 01-Feb-2002 #text_change 01-Feb-2002
C, Accessi	C; Accession: A59406; S56749
R;Ozaki,	R;Ozaki, H.; Ishii, K.; Horluchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; I
J. Immunc	01. 163, 553-557, 1999
A; Title:	A; Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma Causes redistribut:
A; Referen	A; Reference number: A59406; MUID: 99323940; PMID:10395639
A; Access:	A; Accession: A59406
A;Status:	A;Status: preliminary
A;Molecul	A; Molecule type: DNA
A;Residue	A;Residues: 1-299 <oza></oza>
A;Cross-1	A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R, Naik, U	R; Naik, U.P.; Bhrlich, Y.H.; Kornecki, E.
Biochem.	J. 310, 155-162, 1995
A; Title:	Mechanisms of platelet activation by a stimulatory antibody: cross-linking of i
A;Refere	A;Reference number: S56749; MUID:95374438; PMID:7646439
A; Access:	ion: 856749
A; Molecu.	A; Molecule type: protein
A;Residu	es: 20-49,'X',51-53,62-73,'B',75-103,123,'P',125-130,'FDKDXTIYLNXY';'LT',206,'X
A; Note:	A; Note: the order of the peptides other than the amino terminus was not determined
C; Genetics:	CB:
A; Gene: JAM	JAM
C; Keywor	C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet memblane
P;1-25/D	P;1-25/Domain: signal sequence #status predicted <sig></sig>
P;26-299,	P;26-299/Product: junctional adhesion molecule #status predicted <mat></mat>
vrain	Match 25.4%; Score 415; DB 2; Length 299;
Best L	
Matche	Matches 100; Conservative 50; Mismatches 132; Indels 14; Gaps 6;
ò	18 PPILILERGCMIEAVNLKSSNRNPVVHEPESVELSCIITHSQTSDPRIEWKIQDGQTTY 77
qa	15 PILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWKFDQGDTTRL 72
è	78 VYPNNKINGDIAGRIDVRGKTSLRIWNVTRSDSALYRCEVVALNDRKEVDBITIBLIVQV 137
Š	

Gaps

34;

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A,Accession: A39712
A,Status: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-1051 (CHO>
A,Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C,Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoly
                                                                                                                                                                                                                                                   F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbobydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A;Title: Characterization of a member of the immunoglobulin gene superfamily that possi
A;Reference number: A39712; MUID:91271300; PMID:1711213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 V--CRIPAAVPVGKTATLQCQBSEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 ARQLRVNATANMAESVVLSC-DADGPPDPEISWLKKGEPIEDGE------EKISF--NED 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 KVSRSDSGNYTC--IASNSPOGBIRATVOLVVAVYVTPKGRPBPTTVYOGHTAMPOCQ-A 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DA------GAARCEGODMEV-YD-LNIAGIIGGVLVVLIVLAVITMGICCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCNIKHREAPLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIIIVLGLMPYCKK 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Gallus gallus (chicken)
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 VNLKIYOKLTFKNAPTPQBPXEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCB--VVALNDRKGVDBITIBLIVQVKPVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BGYPRPHYSWYRNDVPLPTDSRANPRPQNSSPHVNSBTGTLVFNAVHKDDSGQYYCIASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 NVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 VNLK-----SSNRNPVVHBPESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYPDNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 BP-ESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRIDVFGKTSLRIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597 EGDPVPHIQWKGKDKIL-DPSKLLPRIQ-----IMPNGSLVIYDVTTEDSGKYTCIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1051;
                                                                                                                                                                                                                                                                                                                                                                     Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                       81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                    fibronectin type III repeat homology <FN3A>
fibronectin type III repeat homology <FN3B>
transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.9%; Score 178; DB 2; L
Llarity 28.3%; Pred. No. 2.1e-06;
Conservative 29; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 180; DB 1;
28.8%; Pred. No. 1.5e-06;
tive 33; Mismatches 91;
immunoglobulin homology <!MM2>
heparin binding #status predicted
heparin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P;775-1046/Domain: protein kinase homology <KIN>P;783-791/Region: protein kinase ATP-binding motif
                                                                                  immunoglobulin homology <IRM4>
immunoglobulin homology <IRM4>
immunoglobulin homology <IRM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 QSEMTIHHVEKDDEAEYSCIANNQAGEA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: ATP
P;775-1046/Domain: protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase-like protein klg precursor
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 72; Conserv
                             P;149-153/Region: b
P;158-162/Region: b
F;25-284/Domain: ii
F;317-381/Domain: ii
P;413-475/Domain: ii
P;512-589/Domain: f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: A39712
  F;129-188/Domain:
                                                                                                                                                                                                 F;618-679/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
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                                                                                                         Nitternate names: NCAM-180

Nitternate names: NCAM-180

Nitternate names: NCAM-180

NiContains: neural cell adhesion molecule, short domain form (NCAM-140)

Cipace: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

A;Kitle: Primary structure and developmental expression of a large cytoplasmic domain fc

A;Residues: 17-1088 KRI:

A;Residues: 1-1088 KRI:

A;Cross-references: EMBL:MD5696; NID:g214609; PIDN:AA49909.1; PID:g214610

A;Note: the authors translated the codon AAA for residue 970 as Leu

C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM

C;Comment: NCAM mediates cell-cell adhesion molecule; fibronectin type III repeat homology; immu

C;Genetics:

A;Gene: NCAM

C;Genetics: alternative splicing; brain; cell adhesion; duplication; heparin binding; si

C;Comment: signal sequence #status predicted <SIG>

F;10-1086/Product: neural cell adhesion molecule, short domain form #status predicted <LE

F;20-1087/Domain: signal sequence = status predicted <EMT>
F;30-705/Domain: immunoglobulin homology <IMMI>
F;34-95/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSB 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 ARQLRVNATAKWAESVVLSC-DADGPPDPBISWLKKGBPIEDGB-----EKISF--NED 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNLKIYQKLTFKNAPTPQBFKEGBDAVIICDVSSSIPSIITWRHKGKD-----VIFKKDV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE - - VVALNDRKGVDBITIBLIVQVKPVTP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural cell adhesion molecule long domain form precursor - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNLK-----SSNRNPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
        251 GILVPGIWPAYSRGHFDRTKKGTSSKK-----VIYSOPSARSBGEFKQTSSFLV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.1%; Score 181; DB 2; Length 725; Best Local Similarity 28.8%; Pred. No. 7.8e-07; Matches 60; Conservative 33; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 QSEMTIHHVEKDDEAEYSCIANNQAGEA 291
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A; Molecule type: mRNA
A; Residues: 1-725 <BAR>
A; Residues: 1-725 <BAR>
A; Residues: 1-725 <BAR>
A; Cross-references: EMBL: Y00051; NID: 953342; PIDN: CAA68263.1; PID: 953343
R; Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A; Title: Difference in aplicing and alternative polyadenylation generates distinct NCAM the Reference number: S00382; MUID: 88283628; PMID: 3396534
A; Accession: S00382
                                                                                                                                                                                                                                                            F;529-606/Domain: Fibronectin type III repeat homology <FN3A>
F;635-695/Domain: Fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TMM>
F;742-739/Domain: intracellular #status predicted <ITMT>
F;740-96,139-189,235-288,330-336,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonter EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
103 GTQSRATVNVKIFQKIMFKNAPTPQRFKEGEDAVIVCDVVSSLPPTIIWK--HKGR---- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 YPDNKIQGDLAGRIDVFGKISLRIMNVIRSDSAIYRCB--VVALNDRKEVDBITIELIVQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 VPPTVQARQSIVNATANIGQSVTLVC-DADGFPERTMSWTKDGBPIENEE-----BDDB 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse NyAlternate names: NCAM-120 C;Species: Wam musculus (House mouse) C;Date: 31-Mar-1993 #text_change 31-Dec-2000 C;Accession: A29673; S00382; A44290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 GCMIEA-VNLKSSNR-----NPVVHEFESVELSCIITHSQTS-DPRIBWKKIQDGQTTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 FHV-NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 KHIFSDDSSELTIRNVDKNDBAEYVCIAENKAGE-----QDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.6%; Score 172.5; DB 1. Best Local Similarity 27.1%; Pred. No. 4.7e-06; Matches 61; Conservative 43; Mismatches 84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132-191/Domain: immunoglobulin homology <IFMU2>
132-156/Region: heparin binding #status predicted
151-156/Region: heparin binding #status predicted
1228-290/Domain: immunoglobulin homology <IFMU3>
2563-272/Region: NCAM binding #status predicted
132-394/Domain: immunoglobulin homology <IFMU4>
1430-492/Domain: immunoglobulin homology <IFMU4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 642-65,'Di,658-725 <BA2>
A;Crosi-references: EMB:X07195
R;Rougon, G.; Marshak, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A29673
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                                                                                                                                                                                                                                                                                                        C;Species: Drosophila melanogaster
C;Date: 18-Ot-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from Dr
A;Reference number: A31923; MUID:89028670; PMID:3141062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: mRNA
A.Residues: 1-889 «SMA»
A.Residues: 1-889 «SMA»
A.Cross-references: ENEBL:X06564
R.Small, S.J.; Akeson, R.
C. Cell Biol. 111, 2089-22096, 1990
A.Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A.Reference number: A37795; MUID:91035620; PMID:1699951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C;Species: Rattus norvegicus (Norway rat)
C;Dacies: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: 500846; B37795; Ī58136
R;Small, S.J.; Shull, G.B.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence for A;Reference number: $00846; MUID:88059265; PMID:3680385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 KTATLOCOESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFNAVHKDD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 HSAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEED 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 KSSNRNPVVHEFESVELSCIITHSQ-TSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTD 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-333 <SEE>
A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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;; Pred. No. 6.7e-07;
38; Mismatches 82; Indels
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                                                                                                                                                                                                                                                                                   amalgam protein precursor – fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.2%;
Matches 53; Conservative 36
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                                                                                          |: : :||
710 RRKAKRLKKHPEGB 723
                                                     267 YRRGCFISSKQDGB 280
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A;Residues: 340-381 <SM2>
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A; Accession: A44290
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NyAlternate names: NCAM-180
NyAlternate names: NCAM-180
NyContains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C; Species: Mus musculus (Duouse mouse)
C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C; Accession: A29673; S00844; S00384; A42290; S00383
R; Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A; Fitle: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,00d
A; Reference number: A29673; MUID: 87246524; PMID: 3595563
A; Accession: A29673; MUID: 87246524; PMID: 3595563
A; Accession: A29673; MUID: 87246524; PMID: 359563 1; PID: 555599, F, 601, L, A; Ross - references: EMBL: V00051; NID: 953342; PIIN: CAA68263 1; PID: 955343
A; Accession: A29673; MUID: 88067687; PMID: 3684567
A; Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur
A; Reference number: S00844; MUID: 88067687; PMID: 3684567
A; Accession: S00844
A; Molecule type: mRNA
A; Residues: 529-809, 1077-1115 <SAN>
A; Cross - references: EMBL: X06328; NID: 953322; PIDN: CAA29641.1; PID: 9817984
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Molecule type: protein
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fi132-191/Domain: immunoglobulin homology Fi132-191/Domain: immunoglobulin homology Fi132-191/Domain: immunoglobulin homology Fi132-156/Region: heparin binding #status predicted
Fi28-290/Domain: immunoglobulin homology Fi180-290/Domain: fibronectin type III repeat homology Fi180-290/Domain: fibronectin type III repeat homology Fi180-290/Domain: fibronectin type III repeat homology Fi180-290/Domain: fibronectin cype III repeat homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-98/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 YFDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDBITIBLIVQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCMIEA-VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 169.5; DB 1
Similarity 27.7%; Pred. No. 6.8e-06;
2; Conservative 43; Mismatches 84.
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A; Introns: 701/1
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A Map position: 9
A. Map position: 9
A. Introns : 643.3; 701/1; 770/2; 808/2; 1076/2
C. Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; imm C. Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s C. Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s F.1-19/Domain: signal sequence #status predicted (510-87)
F. 20-811/Product: neural cell adhesion molecule, long domain splice form #status exper F. 20-819,1077-1115/Product: neural cell adhesion molecule, short domain splice form #st. 20-711/Domain: extracellular #status predicted (5XT)
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                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 642-1115 <BAR>
A,Cross-references: EMBL:X07195
R;Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A,Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A,Reference number: A28281; MUID:88247737; PMID:2454455
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F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
BMBO J. 7, 625-632, 1988
Affitle: Differential splicing and alternative polyadenylation generates distinct NCAM
A;Reference number: S00382; MUD:88283628; PMID:33396534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the amino-terminal domain
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A;Residues: 804-1081 <BA3>
A;Cross-references: BMBL:X07244; NID:953321; PIDN:CAA30230.1; PID:9929720
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J. Biol. Chem. 251, 3395-3401, 1986
A;Title: Structural and immunological characterization of A;Title: Structural and immunological characterization of A;Reference number: A44290; MUID:86140120; PMID:3512556
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1312-191/Domain: immunoglobulin homology <IRM1>
1312-191/Domain: immunoglobulin homology <IRM2>
1312-191/Domain: immunoglobulin homology <IRM3>
1328-290/Domain: immunoglobulin homology <IRM3>
1328-290/Domain: immunoglobulin homology <IRM4>
1321-388/Domain: immunoglobulin homology
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jacession: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999; A21917; B31917; S66460; A210010: D.M.; Pulle, A.; Valente, P.; Cai, S.; Horigan, B.; Sasaki, M.; Yamada, Y.; H.; Noonan, D.M.; Pulle, A.; Valente, P.; Cai, S.; Horigan, B.; Sasaki, M.; Yamada, Y.; H.; Boll, Chem. 266, 22939-22947; 1991.
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, Kaedidues; 1-3707 cNOD.
; Kredidues; 1-3707 cNOD.
; Kredidues; 1-3707 cNOD.
; Kredidues; 1-3707 cNOD.
; Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hası
BAld. Chem. 283, 16379-16387, 1988
BAld. Chem. 283, 16379-16387, 1988
; Title: Identification of CDNA clones encoding different domains of the basement membr; Reference number: A92680; MUID:89034110; PMID:2972708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA AND: AND: ARRAMAND PIDN: AAA39912.1; PID: 9200301
A; Residues: 1870-2600 AND: ARRAMAND ARA39912.1; PID: 9200301
A; Cross-references: GB: J04055; NID: 9200300; PIDN: AAA39912.1; PID: 9200301
R; Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
R; Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
A; Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
A; Title: Structural properties of recombinant domain III-3 of perlecan containing a glo! A; Reference number: S66460; MUID: 95377282; PMID: 7649154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Circular 17. Circular 17. Circular 2010 Circular 17. Circular 17. Circular 17. Circular 17. Circular 17. Circular 27. Circ
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;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
;Superfamily: LDL receptor ligand-binding repeat homology; BGF homology; laminin G rep
P;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 -----RPUVLANNYLQIRGIKKTDEGNYRCEGRILA---RGEINYKDIQVIVNVPPPLIQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 QGDLAGRTDVPGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDBITIELIVQVKPVTP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 V--CRIPAAVPVGKTATLQCQBSBGYPRPHYSWYRNDVPLPTDSRANPRPQNSSFHVNSB 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 ARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPIEDGE-----EKISF--NED 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 VNLKIYQKLIPKYAPIPQBPIBGBDAVIICDVSSSIPSIIIWRHKGKD----VIPKKDV 161
                                                                                                                                                                                                                                                                                                                                      32 VNLKSSNR----NPVVHRPESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
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;Residues: 940-1601 <NO2>
;Cross-references: GB:JO4054; NID:g200252; PIDN:AAA39899.1; PID:g200253
;Accession: B31917
                                                                                                                                                                                                                               82; Indels 34;
                                                                                                      Length 1092;
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                                                                                                            10.3%; Score 169; DB 1; 28.4%; Pred. No. 1.2e-05;
                                                                                                                  Query Match 10.3%; Score 169; DB Best Local Similarity 28.4%; Pred. No. 1.2e-Matches 59; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TGTLVFNAVHKDDSGQYYCIASNDAGAA 228
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A;Title: Two neural-cell adhesion molecule(NCAM)-encoding genes in Xenopus laevis are ex
A;Reference number: JN0635; MUID:93273239; PMID:7684721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu ; Superfamily: neural cell adhesion molecule; duplication; heparin binding; sialoglyc;1-19/Domain: signal sequence #status predicted <SIG>
;20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
;20-705/Domain: extracellular #status predicted <EXT>
;30-705/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Comment: This protein mediates and regulates various cell-cell interactions through bc, Stuperfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu;413-475/Domain: immunoglobulin homology <IRMs;512-589/Domain: fibronectin type III repeat homology <3PRs
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Residues: 1-1092 < rmo.
Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
                                    NATIONAL MATERIA DE LA CAMA SURVEY STATE OF LA CAMA STATE OF C
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Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
Accession: JN0638
Toniseen, K. F.; Krieg, P.A.
ene 127, 243-247, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 VNLKSSNR-----NPVVHEFESVELSCIITHSQTSDPR-IEWK-KIQDGQTTYVYFDNKI
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P;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
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149-153/Region: heparin binding #status predicted
158-162/Region: heparin binding #status predicted
1317-381/Domain: immunoglobulin homology <IMM3>
1317-281/Domain: immunoglobulin homology <IMM4>
1512-589/Domain: fibronectin type III repeat homology <FW3A>
1519-680/Domain: fibronectin type III repeat homology <FW3A>
1705-723/Domain: transmembrane #status predicted <IMM>
cell adhesion molecule 2 - African clawed frog
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Gaps

78;

Length 483;

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159 OCOBSEGYPRPHYSWYRNDVPLPTDSRANPRFONSSFHVNSETGTLVFNAVHXDDSGQYY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 CIASNDAGAARCEGQDMEVYDLNIAGIIG------GVLVVLIVLAVI---TMGICCAY 267
                                                                                                                                                                                                                                                                                                          51 LSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGR------TDVPGKTSLR 101
                                                                                                                                                                                                                                                                                                                                                                                                   102 IMNVTRSDSALYRCEVVALADRKEVDELTIELIVQVKPVTPVCRIP---AAVPVGKTATL 158
                                                                                                                                                                                                                                                                                                                                                    8 LECAATCH--PNPQIAWQK--DGGTDPP-----AARERRMHVMPDDDVPFITDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 RRGCFISSKQDGBSYKSPGKHDGV-----NYIRTSBEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q-----TRKKSBEYSVINIDETWVPPDVPSYL--SSQGTLSDRQETWV 247
                                                                                                                                                                                                             Query Match 10.2%; Score 166; DB 2; Length 48
Best Local Similarity 22.8%; Pred. No. 8.1e-06;
Matches 66; Conservative 44; Mismatches 101; Indels
                                                                                      A;Cross-references: EMBL.Ail17666
A;Experimental source: adult uterus; clone DKFZp58601624
C;Genetics:
A;Note: DKFZp58601624.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-483 <DUB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: T17A3.10
A; Accession: T17346
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Best Local S
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A;Nap position: 1
A;Introne: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1;
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3936 VK------PAVVTVGETAVLEGKIS-GKPKPSVKWYKNGEELKPSDRV--KIEN---- 3980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2859 ------TIIRIAHVBLADAGQYRC---AATNAAGTTQSHVLLLVQALPQIS 2900
                                                                                                                                                                                                                                                                                                                       2901 TPPEIRVPA----GSAAVFPCMAS-GYPTPAITWSKVDGDLPPDSRL------ 2942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                           83 KIQCDLAGRIDVFGKISLRIWNVIRSDSAIYRCEVVALADRKEVDBITIELLIVQVKP--- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-6642 <DUZ>
A;Residues: 1-6642 <DUZ>
A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
A;Experimental source: strain Bristol N2; clone C09D1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 RIDVFCKTSLRIMNYTRSDSALYRCE------VVALADRKGVDBITIELIVQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 VKPVTPVCRIPAAVPVGKTATLACQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSFH 196
                                                                                                                                                                                                                                                                                       140 VTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSPHVNS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 EPESVELSCIITHSQTS-----DPRIEWKKIQDGQ----TTYVYFDNKIQGDLAG 90
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hypochetical protein DKPZpS86O1624.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999

C;Accession: T17346

R;Duesterhoofft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. aubmitted to the Protein Sequence Database, September 1999

A;Reference number: Z18727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein UNC-89 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T29757
R;Du, Z; Le, T.T.; Wilson, R.
R;Du, Z.; Le, T.T.; Wilson, R.
R;Du, Z.; Le, T.T.; Wilson, R.
R;Du, Z; Le, T.T.; Wilson, R.
R;Decension: T29777
A;Reference number: Z20679
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
                                                                                                32 VNLKSSNRNPVVHBPESVELSCIITHSQTSDPRIEWKK-----IQDGQTTYVYPDN
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                                                 61;
  Length 3707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 6642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Indels
10.3%; Score 167.5; DB 2; Length 3
26.2%; Pred. No. 6.6e-05;
tive 26; Mismatches 68; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 10.3%; Score 167.5; DB 2
1 Similarity 27.1%; Pred. No. 0.00013;
57; Conservative 30; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2943 ENIMIALPSVRPEDAGTYVCTATNRQGKVK 2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 VNSETGTLVFNAVHKDDSGQYYCIASNDAG 226
                                                                                                                                                                                                                                                                                                                                                                                     200 ETGTLVFNAVHKDDSGQYYCIASNDAGAAR 229
                                                 Conservative
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                 55;
Query Match
Best Local S
Matches 55
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A;Cross-references: EMBL:AP078787; PIDN:AAC26956.1; GSPDB:GN00021; CBSP:T17A3.10 A;Experimental source: strain Bristol N2; clone T17A3 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 LRIW---NVTRSDSAIYRCEVVA--LNDRKEVDBITIELIVQVKPVT----PVCRIPAAV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 PVGKTA---TLOCOESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 PNCKSSIBIRIQCNIT-GHPLPEYSWVTDB-------SSGSTLTIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 VHBPESVELSCIITHSQTSDPRIEWK---KIQDGQTTYVYPDNKIQGDLAGRIDVPGKTS 99
Appointment of protein T17A3.10 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 (C; Accession: T343.3 R; Clarke, K.; Rohlfing, T.; Morris, M. submitted to the RMEL Data Library, July 1998 A; Description: The sequence of C. elegans cosmid T17A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 VYEQDTVNLPCAIPHS----AINWKVSWRLENSNST-----SDLSVTTLIDGNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%; Score 164.5; DB 2; Length 3!
22.8%; Pred. No. 7.4e-06;
tive 57; Mismatches 65; Indels
                                                                                                                                                                                                               A; Accession: T33433
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-352 < CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 3
A;Introns: 21/3; 112/3; 195/2; 341/2
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Search completed: June 15, 2004, 11:05:46 Job time : 16 secs
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Heavral cell adhesion molecule short domain form precursor - bovine

N;Alternate names: NCAM-140

C;Species: Bos primigenius taurus (cattle)

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999

C;Accession: A32976; A38778; B44290; 805402

R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki PEBS Lett. 254, 69-73, 1989

A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and A;Reference number: A12976; MUID:89378239; PMID:2776887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Residues: 20-36 < ROU>
C; Comment: S1-Glu was also found
C; Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C; Comment: Various forms of NCAM are produced by alternative splicing.
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C; Reywords: alternative splicing; brain; cell adhesion molecule, short domain form #status experimental F; 1-19/Domain: extracellular #status predicted < REXT>
F; 20-78/Domain: immunoglobulin homology < IMM2>
F; 122-19/Domain: immunoglobulin homology < IMM2>
F; 122-19/FRegion: heparin binding #status predicted
F; 156/Region: heparin binding #status predicted
F; 156/Region: heparin binding #status predicted
F; 156/Region: heparin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
M; Molecule type: protein
M; Residues: 20-3551-61,113-117,122-147,155-161;262-275,279-302;353-360;369-382;544-562;
A; Residues: 20-3551-61,113-117,122-147,155-161;262-275,279-302;353-360;369-382;544-562;
A; Note: the authors identified this protein as calmodulin-independent adenylate cyclase
R; Rougon, G.; Marshak, D.R.
B; R; Rougon, G.; Marshak, D.R.
A; Biol. (Chem. 264, 3386-3401, 1986
A; Title: Structural and immunological characterization of the amino-terminal domain of many R; Reference number: A44290; MUID:86140120; PMID:3512556
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F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transembrane #status predicted <TMM>
F;738-853/Domain: intracellular #status predicted <TNT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 CYVTAEDGTESEATVAVKIFOKLAPKNAPTPOBPREGEDAVIVCDVVSSLPPTIIWK--H 153
            -----RYVEVNVTGSHRKALGFYIIVALLMSV-TVGV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 DGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCB--VVALNDRKBVDBI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TIELIVQVKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRAN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-NAEGFPEPTVSWTKDGEQIENE--- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 CMIEA------VNLKSSNR-----NPVVHEPESVELSCIITHSQTS-DPRIEWKKIQ 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-833 <LIP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
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les 85; Indels
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P;261-270/Region: NCAM binding #status predicted
P;321-396/Domain: immunoglobulin homology <IPM4>
P;428-490/Domain: immunoglobulin homology <IPM4>
                                                                                  264 CCAYRRGCFISSKQ--DGESYKSPGKHD 289
                                                                                                                                    325 C-----VFLISERVANGTEKKRPVQYN 346
    ----BDSGVFQCIDSKN----
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 15, 2004, 10:51:49; Search time 10 Seconds (without alignments) 1614.175 Million cell updates/sec

US-09-524-531C-13 1633 1 MALSRRIELKLYARLPHFFL........VNYIRTSEEGDFRHKSSFVI 310

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	dı	JAM2 HUMAN	JAM1 MOUSE	JAM1_HUMAN	JAM1_BOVIN	A33 HUMAN	NCAI XENLA	PTK7_CHICK	AMAL DROME	CXAR HUMAN	NCM2 MOUSE	NCA1 RAT	LACH_SCHAM	NCA2 MOUSE	NCA1 MOUSE	NCA2_XENLA	NCM2 HUMAN	PGBM_MOUSE	UN89_CAERL	NCAL BOVIN	NTRI HUMAN	NCA2_HUMAN	NCA1 HUMAN	NEO1_RAT	CAML_FUGRU	NCA1_CHICK	NTRI MOUSE	NTRI_RAT	NEO1 MOUSE	CEPU_CHICK	CXAR_MOUSE	FAS2_DROME	PTPD_HUMAN	SN_MOUSE
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P98160 homo sapien Q13308 homo sapien Q92859 homo sapien Q02246 homo sapien P22063 rattus norv P20273 homo sapien Q2472 drosophila P06731 homo sapien P31809 mus musculu Q90610 gallus gall P11834 bos taurus P32736 rattus norv
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## ALIGNMENTS

RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LSRRIRLRLYARLPHFFLLLLFRGCMI-----RAVNLKSSNRNPVVH--BFBSVELSCII 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARRSRHRL-----LLLLLRYLVVALGYHKAYGPSAPKDQQVVTAVBYQBAILAC-K 51
FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENUTLES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                      SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. DATABASE: NAME=PROW, NOTFS=PROW 2:1-3(2001); WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
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JUNCTIONAL ADHESION MOLECULE 2.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.9%; Score 505; DB 1; Length 298
37.3%; Pred. No. 9.7e-36;
tive 61; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. . .) (PA
CA78E518E22DCAEE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005887; C:integral to plasma membrane; NAS. GO; GO:0016337; P:cell-cell adhesion; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_c2.
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IG-LIKE C2-TYPE.
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298 AA;
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MEDINE-21391702; PubMed=11500366;

MEDINE-21391702; PubMed=11500366;

Mostrewa D., Brockhaus M., D'Arcy A., Dale G.B., Nelboeck P.,
Schmid G., Mueller F., Bazzoni G., Dejana B., Bartfai T.,
Minkler F.K., Hennig M.;
Minkler F.K., Hennig M.;

"X-ray structure of junctional adhesion molecule: structural basis for mopphilic adhesion via a novel dimerization motif.";

I MMO. J. 20:4391-4398 (2001).

I FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.

Involved in platelet activation.

Involved in platelet activation.

SC -1- SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98127120; PubMed=9660867;
Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
Simmons D., Dejana E.,
"Junctional adhesion molecule, a novel member of the immunoglobulin
superfamily that distributes at intercellular junctions and modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interaction.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH PARD3.

MEDLINE=21340266, PubMed=11447115;
Ednet K., Suzuki A., Horikoshi Y., Hirose T.,
Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
Mithe cell polarity protein ASIP/PAR-3 directly associates with junctional adhesion molecule (JAM).";
EMBO J. 20:3738-3748(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelial and endothelial cells.
--- SIMILARITY: Belongs to the immunoglobulin superfamily.
--- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: Localized at tight junctions of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Inductional adhesion molecule 1 precursor (JAM)
FIIR OR JAMI OR JCAMI OR JCAM.
                                                                                                                                       300 AA
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocyte transmigration.";
J. Cell Biol. 142:117-127(1998).
                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
283 TTMSENDFXHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U89915; AAC32982.1; -.
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1F97; 22-AUG-01.
MGD; MGI:1321398; F11r.
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                     JAM1_MOUSE
088792;
                                                                                                             JAM1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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75 TTYVYPDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCEVVALADRKGVDEITIELI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGBYTC-MVSEGGQNYGEVSIHLT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 SFHVNSETGTLVPNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 VQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPT-DSRANPRFQNS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LIFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 LIVLAVITMGICCAYRRGCFISSKQDGBSYKSPGKHDGVNYIRTSBEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 LILIGELIFGVWFAYSRGYPETTKKG----TAPGKKVIYSQPSTRSBGEFKQTSSFLV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LLLLFRGCMIBAV-----NLKSSNRNPVVHBPESVELSCIITHSQTSDPRIEWKKIQDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99223940; PubMed=10395639; Ozaki H., Ishli K., Horiuchi H., Arai H., Kawamoto T., Okawa K., Ivamateu A., Kita T.; Combined treatment of TNP-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";
       InterPro; IRR00110; Ig-like.
InterPro; IRR00110; Ig-like.
InterPro; IRR00110; Ig-like.
InterPro; IRR00110; Ig-like.
PROMO47; ig. 2.
PROSITE; PSS00835; IG_LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; 3D-structure.
IGNAL.
Inchart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 43, Last annotation update)
Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion molecule 1) (Platelet Fil receptor) (UNQ264/PR0301).
PIIR OR JAM1 OR JCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and sequencing of the cDNA of F11 receptor, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
Kornecki E.;
                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
391F3E48FF3B97EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                  27.5%; Score 449.5; DB 1; Length 300; 34.2%; Pred. No. 5.2e-31; ive 64; Mismatches 117; Indels 15
                                                                                                                                                                      JUNCTIONAL ADHESION MOLECULE 1.
                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                               IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 AA
GO:0005515; P:protein binding; IPI.
                                                                                                                                                                                                          POTENTIAL
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    Immunol. 163:553-557(1999).

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                                                                                                                                                                      (Human)
                                                                                                                                                                                                        239
260
260
134
152
162
185
300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 102; Conserv
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Q9Y6Z4;
                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SRQUENCE
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Matches
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Junctional adhesion molecule 1 precursor (JAM)
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TRANSMEM
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DOMAIN
DISULPID
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 VYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDBITIELIVQV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 KPVTPVCRIPAAVPVGKTATLOCORSEGYPRPHYSWYRNDVPLPIDSRANPRFONSSPHV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCBGQ-DWEVYDLNIAGIIGGVLVVLIVL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 FFLLLLFRGCMIRAVNLKSSNRNPVVHBFRSVELSCIITHSQTSDPRIEWKKIQDGQTTY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 AVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTS--EEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
D95DE2FEA23D2851 CRC64;
  SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                     JUNCTIONAL ADHESION MOLECULE 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                25.4%; Score 415; DB 1; Length 299; 33.8%; Pred. No. 4.4e-28; tive 50; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                          POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
                                                                                                                                                                                                   GO; GO:0005911; C:intercellular junction; TAS.
GO; GO:0006954; P:intlammatory response; TAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                          EMBL, AP111713; AAD42050.1; -.
EMBL, AP207907; AAF22829.1; -.
EMBL, AL136649; CAB66584.1; -.
EMBL, AY358996; AAQ8255.1; -.
EMBL, AY358996; AAQ8255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               32583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                       PIR; A59406; S56749.
Genew; HGNC:14685; F11R.
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299
238
238
259
259
228
228
212
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                                                                                                                                                                                                                                          Pfam; PF00047; 19; 2.
                                                                                                                                                                                                                                                                                                      26 26 26 26 26 26 26 27 1135 21 153 21 185 185 185 299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                    Repeat; Signal signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
10-OCT-2003
                                                                                                                                                                                           MIM; 605721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JAMI BOVIN
ID JAMI BOVIN
AC Q9XT56;
                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
DOMAIN
DOMAIN
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DISULPID
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 QVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSF 195
                                                                                                                                                                                                                                                                                                                    "Combined treatment of TMF-alpha and IFM-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.";

"Combined treatment of 1535-557(1899).

"I Immunol. 163:153-557(1899).

"I FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of FARD3 with JAMI, thereby preventing prevent the interaction of PARD3 with JAMI, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier. Involved in platelet activation.

"SUBJUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction (By similarity).

"INSUBJUAR LOCATION: Type I membrane protein (Potential).

"INSUBJUARITY: Belongs to the immunoglobulin superfamily.

"INTLARITY: Contains 2 immunoglobulin superfamils.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITR; PSS0835; IG_LIKR; 2.
Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-99323940; PubMed=10395639;
Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
Iwamatsu A., Kita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUNCTIONAL ADHESION MOLECULE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714FE1C1714769A2 CRC64;
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF111714; AAD42051.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32456 MW;
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SMART; SM00408; IGc2; 1.
                                                                                                                      Bovidae; Bovinae; Bos
NCBI_TaxID=9913;
Filk OR JAM1.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 1
152 2
184 1
298 AA;
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mmunoglobulin domain;
                                                                                                                43
             ransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XENLA
                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
                                                                                                                                                     CARBOHYD
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                                                                                                                                          DISULPID
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                             Query Match
                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCA1 XEN
P16170;
                        SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                    VLAVITMGICCAYRRGCPISSKQDGES----YKSPGKHDGVNYIRTSEEGDPRHKSSFVI 310
                                                                                  248 LLGALIFGIWFAYSRGYFDRAKKGTSNKKVIYSQP------NARSDGEFRQTSSFLV 298
LVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSBYKWFKDGVEMPLEPKSNRAPSNSSY 187
                                    HVNSBTGTLVFNAVHKDDSGQYYCIASND-AGAARCEGQDMBVYDLNIAGIIGGVLVVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The human A33 antigen is a transmembrane glycoprotein and a novel member of the immunoglobulin superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).
                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Colon carcinoma;
MEDLINE=97165045; PubMed=9012807;
MEDLINE=87165045; PubMed=9012807;
Moritz R.L., White S.J., Johnstone C.N., Catimel B., Simpson R.J., Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C., Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice B.C., Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of posttranslational modifications of human A33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 602171; -.
GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97396159; PubMed=9245713;
Ritter G., Cohen L.S., Nice B.C., Catimel B., Burgess A.W.,
Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-WAR-2004 (Rel. 43, Last amontation update)
Cell surface A33 antigen precursor (Glycoprotein A33)
                                                                                                                                                     319 AA
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           POST-TRANSLATIONAL MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U79725; AAC50957.1; -.
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:4445; GPA33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Palmitoylated
                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson R.J.;
                                                                                                                                                  A33 HUMAN
Q99795;
                                                                    255
                       196
                                             188
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--IQGDL-----AGRIDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKEVDEITI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 BLIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDV-----PLPTDSRA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 QP------VSLKNISTDTSGYYICTSSNREGTQPCNITVAVRSPSMAVALY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 DINIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDG----BSYKSPGKHDGVNYI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 IEAVNLKSSNRNPVVHBPESVELSCIITHSQTS--DPRIEWKKIQDGQTTYVY---PDNK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 VDAISVETPODVLRASOGKSVTLPCTY-HTSTSSREGLIQMDKLLLTHTERVVIWPPSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 NPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAG------ARCEGQDMEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
Xenopodinae, Xenopus.
NCBI_TaxID=8355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 17:10321-10335(1989).
-1- FUNCTION: This protein is a cell adhesion molecule involved neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..). (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
9BPC7AAP45C2409B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieg P.A., Sakaguchi D.S., Kinther C.R.; "Primary structure and developmental expression of a large cytoplasmic domain form of Kenopus laevis neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 242.5; DB 1; Length 319; 25.7%; Pred. No. 2.3e-13;
Lipoprotein; Palmitate; Glycoprotein;
Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.3e-13;
49; Mismatches 123; Indels
                                                                         CELL SURPACE A33 ANTIGEN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPIASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
POLY-CYS.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180)
MEDLINE-90098871; PubMed=2481269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1088 AA.
                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  35632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.74 tes 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 RTSEEGDFRHK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                               Signal;
                                                                                                                                                                                                                                                                                                                                        112
200
223
319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecule (NCAM).";
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143 V--CRIPAAVPVGKTATLOCOESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSE 200

85 QGDLAGRIDVFGKISLRIWNVIRSDSAIYRCE - - VVALNDRKEVDEITIBLIVQVKPVTP 142

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                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                        Isoid=P16170-2; Sequence=VSP 002589;
TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURAL CELL ADHESION MOLECULE 1, 180 kDa
                                                                                                                DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                       SIMILARITY: Contains 5 immunoglobulin-like C2-type domains SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform N-CAM 140).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 180; DB 1; Length 1088; 28.8%; Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | G-LIKE C2-TYPE 1. | G-LIKE C2-TYPE 2. | G-LIKE C2-TYPE 2. | G-LIKE C2-TYPE 3. | G-LIKE C2-TYPE 3. | G-LIKE C2-TYPE 5. | G-LIKE C2-TYPE 5. | FIBRONECTIN TYPE-III 1. | FIBRONECTIN TYPE-III 1. | HEPARIN-BINDING (POTENTIAL). |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62738B55B03F3E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; 2.
SMART; SM00408; IGc2; 5.
PROSITE; PSSOB35; IG LIKE; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat;
Immunoglobulin domain; Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
SUBCELLULAR LOCATION: Type I membrane protein.
                          Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                    IsoId=P16170-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTIG=VSP
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N-LINKED (
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                                                                                                                                                                                                                                                                                                                            HSSP; P56276; ITLK.
InterPro; IPR008957; FN_III-like.
InterPro; IPR001961; FN_III.
InterPro; IPR001110; Ig-like.
InterPro; IPR001110; Ig-like.
Pfam; PP00041; fn3; 2.
Pfam; PP00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1088 AA; 117778 MW;
                                                                                                                                                                                                                                                                                                    EMBL; M25696; AAA49909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1088
                                       Name=N-CAM 180
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DOMAIN
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Proc. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).
-!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
THE CATALYTIC ACTIVITY OF TYROSINE KIRASE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA,
THYMUS AND BRAIN. WEAKLY EXPRESSED IN PIBROBLASTS. ALSO EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
-i- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin receptor subfamily.
                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Embryonic brain;
MEDLINE-91271300; PubMed=1711213;
Chou Y.-H., Hayman M.J.;
"Characterization of a member of the immunoglobulin gene superfamily that possibly represents an additional class of growth factor
                                                                                                                                                                                                            30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase-like 7 precursor (Kinase like protein)
                                                  201 TGTLVPNAVHKDDSGQYYCIASNDAGAA 228
                                                                      264 QSEMTIHHVEKDDEARYSCIANNQAGEA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PROGIOS; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00408; IGC2; 4.
PRORIT; R980019; TYRC; 1.
PROSITE; PS50011; PRÖTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Prot kinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39712; A39712.
HSSP; P12931; 1PMK.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M63437; AAA48933.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 7.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN EMBRYONIC LIVER.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                     PTK7 OR KLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor.";
                                                                                                                                                          PTK7_CHICK
ID PTK7_CHICK
AC Q91048;
                                                                                                                                                                                                                                                                                                                                                             Gallus.
                                                                                                                                             RESULT 7
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                                                                                   a
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33; Mismatches

60; Conservative

Matches

Query Match Best Local Similarity

81; Indels 34;

us-09-524-531c-13.rsp

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STRAIN=Oregon-R;
EP-ESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRIDVFGKTSLRIW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 NVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQES 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGYPRPHYSWYRNDVPLPTDSRANPRPQNSSPHVNSETGTLVFNAVHKODSGQYYCIASN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 DA------GAARCEGODMEV-YD-1MIAGIIGGVLVVLIVLAVITMGICCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Pred. No. 3.2e-07;
29; Mismatches 109; Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amalgam protein precursor.

AMA OR BG:DS00276.6 OR CG2198.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;

Neopiera; Endoptera; Arthropoda; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.
                   Signal; Glycoprotein; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 178; DB 1; Length 1051;
Pred. No. 3.2e-07;
                                                                               TYROSINE-PROTEIN KINASB-LIKE 7. EXTRACELLULAR (POTENTIAL).
                                                                                                                                       CYTOPLASHIC (POTENTIAL).

1G-LIKE C2-TYPE 1.

1G-LIKE C2-TYPE 2.

1G-LIKE C2-TYPE 4.

1G-LIKE C2-TYPE 4.

1G-LIKE C2-TYPE 5.

1G-LIKE C2-TYPE 5.

1G-LIKE C2-TYPE 5.

1G-LIKE C2-TYPE 5.

1G-LIKE C2-TYPE 7.

PROTEIN KINASE; INACTIVE.

BY SIMILARITY.

BY SI
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01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
    PROSITE; PS00109; PROTEIN KINASE TYR; 1.
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                     Receptor; Transmembrane; Si
Immunoglobulin domain; Repe
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DOMAIN 23 685
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DOMAIN 707 1051
DOMAIN 23 105
DOMAIN 213 298
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Matches 72; Conservative
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MEDLINE=22426066; PubWed=12537569;
MEDLINE=22426066; PubWed=12537569;
Stapleron M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.B.; Frommiller B., Pacleb J.M., Park S., Wan K.H.,
A Drosophila Full-length cDNA resource.";
Genome Biol. 3.RESBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RESEBARCH0080.1-RES
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Celniker S.B., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
Palazzolo M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence of the Antennapedia complex of Drosophila.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
MEDLINE-89028670; PubMed=3141062;
Seeger M.A., Haffley L., Kaufman T.C.;
"Characterization of amalgam: a member of the immunoglobulin guperfamily from Drosophila.";
Cell 55:589-600(1988).
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Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
                                                                                                                                                                                                                                   Pfam; PF00047; ig; 3. SMART; SM00408; IGc2; 2. PROSITE; PS50835; IG_LIKE; 3. Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
Q -> K (IN REF. 1).
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REMOVED IN MATURE FORM (POTENTIAL)
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 Usage by
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P644753DB3DB25F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
PROBABLE.
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 modified and this statement is not removed.
                    entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                                        PIR; A31923; A31923.
PlyBase; FBgn000071; Ama.
GO; GO:005886; C:plasma membrane; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_C2.
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MEDLINE=97190109; PubMed=9036860;
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24 7 AM
2 333 REE
25 128 IG
139 223 IG
46 117 PRE
161 208 PRE
161 208 PRE
251 307 PRE
46 86 N-1
86 86 N-1
83 83 N-1
333 AA, 36387 MF,
                                                                      EMBL; M23561; AAA28367.1; -.
EMBL; AAE01572; AAD19797.1; -.
EMBL; AE000574; AAE54084.1; -.
EMBL; AX051911; AAK93335.1; -.
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Richanger R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Ra Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ra Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Romanein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Sodergren R.J., Lu X., Gibbs R.A.,

Rahas J. Helton B.K., Retreman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Roderstion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                            Pomko R.P., Xu R., Philipson L.;
"HCAR and MCAR: the human and mouse cellular receptors for subgroup
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- PUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (ADZ AND ADS).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
Sollarbrant K., Sonnhammer B., Philipson L.,
Pertarive regulatory domains in the human and mouse CAR genes.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization and chromosomal localization of the human Coxeackievirus B-adenovirus receptor gene."; Hum. Genet. 105:354-359(1999).
"Isolation of a common receptor for Coxsackie B viruses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P., Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P., "Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor."; Submitted (OCT-1999) to the BMBL/GenBank/DDBJ databases.
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Bowles R.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
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Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
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AF169360; AAF05908.1; JOINED.
AF169361; AAF05908.1; JOINED.
AF169362; AAF05908.1; JOINED.
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MEDLINE=22388257; PubMed=12477932;
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EMBL; U90716; AAC51234.1; -.
                                                    adenoviruses 2 and 5.";
Science 275:1320-1323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                             FROM N.A.
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Name=Long;
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   208 AVHKDDSGQYYCIASNDAGAARCEGQDMBVYDLNIAGIIGGVLV-VLIVLAVITMGICCA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 AAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSFHVNSETGTLVFN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 V-----FCKTSLRIMNVTRSDSAIYRCEVVALNDRKGVDEITIELIVQVKPVTPVCRIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 ESVELSCIITHS-QTSDP-RIEW-----KKIQDGQTTYVYFDNKIQG----DLAGRTD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 BTAYLPCKFTLSPEDOGPLDIEWLISPADNQKVD--QVIILYSGDKIYDDYYPDLKGRVH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 10.6%; Score 172.5; DB 1; Length 365; Similarity 25.9%; Pred. No. 2.5e-07; 68; Conservative 38; Mismatches 116; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCM2_MOUSE STANDARD; PRT; 837 AA.
035136; 035662;
115-JUL-1998 (Rel. 36, Created)
115-JUL-1998 (Rel. 36, Last sequence update)
116-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell adhesion molecule) (K4B12).
NCAM OR OCAM OR RNCAM.
Mus musculus (Mouse).
                                                                                                                                                                                                                             MIM; 602621; ---
GO; GO: 0005887; C: integral to plasma membrane; TAS.
GO; GO: 0004887; C: integral to plasma membrane; TAS.
GO; GO: 0004887; F: C: integral to plasma membrane; TAS.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
SWART; SM00408; Ig_c2: 1.
PROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 CYTOPLASMIC (POTENTIAL).
134 IG-LIKE C2-TYPE 1.
120 BY SIMILARITY.
120 BY SIMILARITY.
106 N-LINKED (GLCNAC. . ) (POTENTIAL).
107 N-LINKED (GLCNAC. . ) (POTENTIAL).
108 AB01C6346CB7FE64 CRC64;
EMBL, AF169363, AAP05908.1; JOINED. EMBL, AF169364; AAP05908.1; JOINED. EMBL, AF169365; AAP05908.1; JOINED. EMBL, AF200465; AAR05908.1; SMBL; AF242865; AAG01088.1; SMBL, AF242865; AAG01088.1; SMBL, AF242864; AAG01088.1; JOINED. EMBL, AF242864; AAG01088.1; SMBL, BC003664; AAG01088.1; JOINED. EMBL, EC010536; AAH10536.1; SMBL, EC010536; AAH10536.1; SMBL, EAM, 09-NOW-00. PDB; IEAM; 09-NOW-00. PDB; IEAM; AG0108.1; SMBL, EAM; AG010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 YRRGCFISSKODGESYKSPGKHD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RK-----KRREEKYEKEVHHD 276
                                                                                                                                                                                                                                                                                                                                                                                            Repeat; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF001287; AAB69125.1; --
REMBL; AF001287; AAB69125.1; --
REMBL; AF001286; AAB69124.1; --
REMBL; AF001286; AAB69124.1; --
REMBL; AF001286; AAB63135.1; --
REMBL; AF001289; Ncam2.
RINterPro; IPR008957; FN III-like.
RINterPro; IPR0013598; Ig_c2.
REMBL; PR00041; finj; 2.
REMART; SM00060; FN3; 2.
REMART; SM00100; FN3; 2.
REMART; SM00101; GIJEKE; 5.
REMOSTER; PS50835; IG_LIKE; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoid=035136-2; Sequence=VSP 002590;
--- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and vomeronasal neurons in a zone-specific manner.
--- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
--- SIMILARITY: Contains 2 fibronectin type III domains.
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                              SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRAIN=BALB/c; TISSUR=01factory neuroepithelium;
MEDLINE=97368238; PubMed=9221781;
YOSHIDHARA Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
Kagamiyama H., Mori K.;
"OCAM: A new member of the neural cell adhesion molecule family
related to zone-to-zone projection of olfactory and vomeronasal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
NEURAL CELL ADHESION MOLECULE 2.
EXTRACELLULAR (POTENTIAL).
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
PIBROMECTIN TYPE-III 1.
PIBROMECTIN TYPE-III 2.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bvent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035136-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE
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837
718
837
108
2297
2297
2396
678
                                          NCBI_TaxID=10090;
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208
302
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401
482
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Event=Alternative aplicing, Named isoforms=1,
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                                                                                                                                                 EMBL; X06564; CAA29809.1; -.
                                                                                                                                                        EMBL; M32611; AAA41679.1; -. PIR; S00846; IJRINC. PDB; 1EPF; 27-OCT-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
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858 AA;
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309
417
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SIGNAL
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CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                  GYPRPHYSWYRNDVPLPTDSRANPRPQNSSFHV-NSBTGTLVFNAVHKDDSGQYYCIASN 223
                                                                                                                                                                                                                                                                                                            GSPDPTISWFRIGKLIB-----ENERYILKGSNTELTVRNIINK-DGGSYVCKAIN 285
                                                                                                                                                                                                                                         130 EDAEVVCRVSSSPA--PAVSW-----LYHNEEVTTIPDNRFAVLANNNLQILNIN 177
                                                                                                                                                                                                                                                           RSDSAIYRCEVVALANDRKEVDBITIELIVQVKP - - VTPVCRIPAAVPVGKTATLQCQBSB 164
                                                                                                TLFNGLGLGAI I GLGVAALLL I LVVTDVSCPFI RQCGLLAC
I TRRMCGKKSGSSGKSKELEEGKAAYLKDGSKEPI VEARTE
                                                                                                                            ETIBIKVSNDIIQSKEDDIKA -> NCCEANKGENGGQSWH
LANAVGFTFVITMSLSCLF (in isoform Short).
                                                                                                                    Deritnhedgspynbpnrttpltepeklplkbengkbylna
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
                                                                                                                                                                                                                                                                               KSDEGIYRCE-GRVEARGEIDFRDIIVIVNVPPAIMMPQKSFNATAERGEEMTLTCKAS-
                                                                                                                                                                                                 Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 355-364 FROM N.A.
MEDLINE=90166485; PubMed=2483093;
Small S.J., Haines S.L., Akeson R.A.;
"Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is developmentally regulated through alternative splicing.";
Neuron 1:1007-1017(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete coding
                                               (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This protein is a cell adhesion molecule involved neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                27;
                                         (POTENTIAL)
                     (POTENTIAL)
                                POTENTIAL)
                                                                                                                                                                             10.6%; Score 172.5; DB 1; Length 837; 30.1%; Pred. No. 7e-07; 1. Indels 27
                                                                                                                                                          70473B053A2D65A5 CRC64;
                                                         (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                 (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB-Brain;
MEDLINE=88059265; PubMed=3680385;
Small S.J., Shull G.E., Santoni M.-J., Akeson R.;
Tidentification of a cDNA clone that contains the sequence for a 140-kD rat NCAM polypeptide.";
J. Cell Biol. 105:2335-2345(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurites, etc.
SUBCELLULAR LOCATION: Type I membrane protein.
THERNATIVE PRODUCTS:
                                                                                         (GLCNAC.
                                (GLCNAC.
                     (GLCNAC
                                                                                                                                                /FTId=VSP 002590
                                                                                                                                                                                                                                                                                                                                                                                                            858 AA
                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                            837 AA; 93203 MW;
                                                                                                                                                                                        Local Similarity 30.1
nes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 380
177
177
219
309
406
419
445
445
837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                         DAG 226
                                                                                                                                                                                                                                                                                                                                                            KÀG 288
 322
422
177
177
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406
419
445
694
694
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NCAM1 OR NCAM.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 YPDNKIQGDLAGRIDVPGKTSLRIWNVTRSDSAIYRCE--VVALNDRKGVDBITIELIVQ 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IRR008951; FN III-like.
InterPro; IRR003961; FN III-like.
InterPro; IRR0031961; FN III.
InterPro; IRR003198; Ig_c2.
InterPro; IRR003198; Ig_c2.
Pfam; PP00041; fd3; 2.
Pfam; PR00047; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00060; FN3; 2.
SMART; SM00060; IG_LIKE; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCMIEA-VNLKSSNR-----NPVVHBPBSVELSCIITHSQTS-DPRIBWKKIQDGQTTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEURAL CELL ADHESION MOLECULE 1, 140 kDa ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                   C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%; Score 172.5; DB 1; Length 858; 27.1%; Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASHIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 7.

IG-LIKE CANAC. (POTENT 7.

IG-LIKE GGCCHAC. (POTENT 7.)

IG-LIKE GGCCHAC. (POTENT 7.)
                                                     "Isoid=P13596-1; Sequence=Displayed;
-i- SIMILARITY: Contains 5 immunoglobulin-like C2-type dc
-i- SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EA1A06A4EA0550F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
Comment=A number of isoforms are produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches
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us-09-524-531c-13.rsp

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Query Match
Best Local S:
Matches 63
               SEQUENCE
  LIPID
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210 VPPTVQARQSIVNATANLGQSVTLVC-DADGPPEPTMSWTKDGBPIKNEB------RDDB 262
                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
TISSUE SPECIFICITY: EXPRESSED BY ALL NEUROCENIC CELLS EARLY, BUT
ONLY THOSE CELLS THAT BECOME NEUROBLASTS CONTINUE TO EXPRESS IT.
EXPRESSED BY NEUROBLASTS, GANGLION WOTHER CELLS AND NEURONS EARLY
IN THEIR LIVES, BUT EXPRESSION BECOMES RESTRICTED TO A SUBSET OF
NEURONS AS DEVELOPMENT PROCRESSES. EXPRESSED BY SENSORY NEURONS AS
THEY DELAMINATE FROM THE BODY WALL ECTODERM. IT IS ALSO PRESENT ON
GROWING AXONS OF THE CNS AND PNS AND BECOMES RESTRICTED TO A
SUBSET OF AXONS LAFTER IN DEVELOPMENT.
BUYGLOPMENTAL STAGE: EXPRESSED ON DIFFERENTIATING NEURONAL CELLS
FROM THE ONSET OF NEUROGENESIS IN BOTH THE CENTRAL AND PERIPHERAL
                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: MAY PLAY A ROLE IN EARLY NEURONAL DIPFERENTIATION AND
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=94038693; PubMed=8223276;
Karletrom R.O., Wilder L.P., Bastiani M.J.;
"Lachesin: an immunoglobulin superfamily protein whose expression correlates with neurogenesis in grasshopper embryos.";
Development 118:509-522(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR07110; 19-like.
InterPro; IPR07110; 19-like.
Pfam; PF00047; 19; 3.
SMART; SM00408; IGG2; 2.
PROSITE; PS06135; IGL LKB; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein.
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IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
POTENTIAL.
                                                                                                                                                                                                                          Bukaryota; Metazoa; Arthropoda; Heapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
NCBI_TaxID=7009;
                          FHV-NSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                                          263 KHIFSDDSSELTIRNVDKNDEABYVCIAENKAGE-----ODASIH 302
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                Schistocerca americana (American grasshopper)
                                                                                                                      349 AA
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HSSP; P80362; IWTL.
                                                                                                                      STANDARD;
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127
218
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15-JUL-1998 (Rel. 36,
10-OCT-2003 (Rel. 42,
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                                                                                                                                                                                        Lachesin precursor.
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DISULPID
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DISULPID
CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                         60 TSDPRIEWKKIQDGQ-----TTYVYPDNKIQGDLAGRIDVFGKT-SLRIWNVTRS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 DSAIYRCEV-VALNDRKEVDEITIELIVQVKPVTPVCRIPA-----AVPVGKTATL 158
                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCAZ MOUSE STANDARD; PRT; 725 AA.
P13594; Q61950;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
                                                                                                                                                                                                                  9 LRLYARLPHFFLLLLFRGCMIRAVNLKSSNRNPVVHEFB-----SVELSCIITHSQ
                                                                                                                                                                                                                                                            159 QCQBSEGYPRPHYSWYR-NDVPLPTDSRANPRFQNSSPHVNSBTGTLVFNAVHKDDSGQY
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                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
a Mr 79,000 polypeptide without a membrane-spanning region.";
EMBO J. 6:907-914 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules."; J. Biol. Chem. 261:3396-3401(1986).
   GPI-anchor amidated glycine (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goridia C.;
polyadenylation generates
in the mouse.";
                                                                                                                                                           74;
                                                                                          Length 349;
                                                                                                                                                       Indels
332 GPI-anchor amidateu yiya...
38974 MW; 5F139A44BF849689 CRC64;
                                                                                          ch 10.4%; Score 170; DB 1; Similarity 25.3%; Pred. No. 3.8e-07; 63; Conservative 39; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88283628; PubMed-3396534;
Barbas J.A., Chaix J.C., Steinmetz M.,
"Differential splicing and alternative
distinct NCAM transcripts and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUB=Brain;
MEDLINE=89251563; PubMed=2721486;
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MEDLINE=87246524; PubMed=3595563;
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Rougon G., Marshak D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 642-725 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 YCIASNDAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 YCVAENGVG 208
   332 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 20-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Mus musculus (Mouse)
 657 (
725 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NCAM-180).
NCAM1 OR NCAM.
 SEQUENCE
                                                                                                                                                                                                                                                                                                                         268
                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL ADHESION MOLECULE 1, 120 kDa
FUNCTION: This protein is a cell adhesion molecule involved in
neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                neurites, etc.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                Isold=Pl3595-2; Sequence=External; SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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Pfam; PF00047; ig; 5.
SWART; SW00060; RN3; 2.
SWART; SW00408; IGC2; 5.
PROSITE; PS50815; IG LIKE; 5.
Cell adhesion; Glycoprotein; Repeat; Alternative splicing; Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> K (IN RBF. 2).
T -> R (IN RBF. 2).
D -> V (IN RBF. 2).
PRE- > SAATEP (IN RBP. 2).
PRE- -> SAATEP (IN RBP. 2).
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HEPARIN-BINDING (POTENTIAL)
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1G-LIKE C2-TYPE 2.

1G-LIKE C2-TYPE 3.

1G-LIKE C2-TYPE 4.

1G-LIKE C2-TYPE 4.

PIBRONECTIN TYPE-III 1.

PIBRONECTIN TYPE-III 2.
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                                                                           Svent=Alternative splicing; Named isoforms=3;
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                                                                                                     Name=N-CAM 180;
IsoId=Pl3594-1; Sequence=Displayed;
IsoId=Pl3595-1; Sequence=External;
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PROBABLE.
PROBABLE.
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EMBL; X15049; CAA33148.1; ALT_SEQ.
EMBL; X07195; CAA33173.1; -.
PIR; A29673; IJMSNG.
PIB; ZNCM; 12-MAR-97.
PDB; 3NCM; 23-JUL-99.
MGD; MGI:97281; NCam1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008957; FW_III-11ke.
InterPro; IPR003961; FW_III.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003598; IG_C2.
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725
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                                                                                           Name=N-CAM 120;
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212
212
309
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SIGNAL
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSS 194
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P13595, Q61949;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
                                                                                                                                                                                                                                                                                                                  103 GTOSEATVNVKIPOKLMPKNAPTPOEPKEGEDAVIVCDVVSSLPPTIIWK--HKGR----
                                                                                                                                                                                                                                                                                                                                                                                         79 YPDNKIQGDLAGRIDVPGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDEITIBLIVQ
                                                                                                                                                                                                                                                  26 GCMIEA-VNLKSSNR-----NPVVHEFESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV
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                                                                                                                                                                               35; Gaps
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Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
"Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000 polypeptide without a membrane-spanning region.";
EMBO J. 6:907-914 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M., Goridis C., Wille W., and Cones that code for the transmembrane forms of the mouse neural cell adhesion molecule (NCAM) and are generated by alternative RNA splicing. "Nucleic Acids Res. 15:8621-8641(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barthels D., Vopper G., Wille W.;
"NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse, is encoded by an alternatively spliced transcript.";
[5] Acids Res. 16:4217-4225(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.; "Differential splicing and alternative polyadenylation generates "Differential splicing and alternative polyadenylation generates Editing."; EMBO J. 7:625-632(1988)
                                                                                                        DB 1; Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SDSSEVTIRNYDKNDEAEYVCIAENKAGB-----QDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 PHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                                                                                                                                                                               Indels
H -> D (IN REF. 2 AND 3).
C2ABB8B4461C6B2F CRC64;
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STRAIN=C57BL/6;
MEDLINE=88067687; PubMed=3684567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
MEDLINE=88283628; PubMed=3396534;
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STRAIN=CS7BL/6J; TISSUB=Brain;
MEDLINE=88247737; PubMed=2454455;
                                                                                                                                      Local Similarity 27.7%; Pred. No. 1e-06; les 62; Conservative 43; Mismatches 84;
                                                                                                                10.4%; Score 169.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOPORM N-CAM 180).
                                         80296 MW;
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NCBI_TaxID=8355;
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                                     DISULFID
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                DISULPID
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InterPro; IRR003951; FM III-like.
InterPro; IRR003951; FM III.
InterPro; IRR003981; FM III.
InterPro; IRR003981; Ig_c2.
Pfam; PR00041; fin3; 2.
Pfam; PR00041; fin3; 2.
SWART; SM0066; FR3; 2.
SWART; SM0060; FR3; 2.
Cell adhesion; Glycoprotein; Transmembrane; Repeat;
Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
                                                                                              SEQUENCE OP 20-36.
MEDLINE=86140120; PubMed=3512556;
Rougon G., Marshak D.R.;
Rougon G., Marshak D.R.;
Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules.";
J. Biol. Chem. 261:3136-34001 (1986).
- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of meurines, etc.
- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEURAL CELL ADHESION MOLECULE 1, 180 kDa
SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
STAIAIN-STAILS
MEDLINE=89251563; PubMed=2721486;
Santoni M.J. Barthels D., Vopper G., Boned A., Goridis C., Wille
"Differential exon usage involving an unusual splicing mechanism
generates at least eight types of NCAM cDNA in mouse brain.";
EMBO J. 8:385-392(1989).
                                                                                                                                                                                                                                                                                                              IsoId=P13594-1; Sequence=External;
SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 fibronectin type III domains.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 5.
FIRRONECTIN TYPE-III 1.
HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                     Svent=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                        IsoId=P13595-2; Sequence=VSP_002588; Name=N-CAM 120;
                                                                                                                                                                                                                                               Name=N-CAM 180;
IsoId=P13595-1; Sequence=Displayed;
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EMBL; Y00051; -: NOT ANNOTATED_CDS.
EMBL; X06328; CAA30471.1; -.
EMBL; X07195; CAA30173.1; -.
EMBL; X07244; CAA30230.1; -.
EMBL; X15051; CAA31150.1; -.
EMBL; X15052; CAA33151.1; -.
PTR; A25673; IJMSNL.
MGD; MGI:97201; NCaml.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 YPDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCE--VVALNDRKEVDBITIELIVQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 VKPVTPVCR--IPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 VPPTVQARQSIVNATANLGQSVTLVC-DADGPPBPTMSWTKDGBPIENERB-DERSKSSV 267
                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                              26 GCMIEA-VNLKSSNR-----NPVVHEFESVELSCIITHSQTS-DPRIEWKKIQDGQTTYV
                                                                                                                                                                                                                                                                      10.4%; Score 169.5; DB 1; Length 1115; 27.7%; Pred. No. 1.8e-06; ive 43; Mismatches 84; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIJINE=9273239; PubMed=7684721;
TODISBEN K.P., Krieg P.A.;
TODISBEN K.P., Krieg P.A.;
TODISBEN K.P., Brieg P.A.;
Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are expressed during development and in adult tissues.";
Gene 127:243-247(1993).

-1- FUNCTION: This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seguence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                             (GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL).
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-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
                                             (POTENTIAL)
                                                                                                                                                                               Missing (in isoform N-CAM 140). /PTId=VSP 002588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SDSSEVTIRNVDKNDEAEYVCIAENKAGE-----QDASIH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 FHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVY 238
                                                                                                                                                                                                                            1115 AA; 119351 MW; 2C93DCD474CFBCAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment=A number of isoforms are produced;
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PROBABLE.
PROBABLE.
N-LINKED
N-LINKED
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N-LINKED
                                                                                                                                                                                                                                                                                                                      62; Conservative
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Best Local Similarity
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 V--CRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSFHVNSE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNLKSSNR-----NPVVHEPESVELSCIITHSOTSDPR-IEWK-KIQDGQTTYVYFDNKI 84
                                                                                                                                                                    Pfam: PP0011; fill; 2.
Pfam: PP00041; fill; 2.
Pfam: PP00047; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00408; IG2; 4.
PROSITE; PS50835; IG_LIKE; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat;
Immunoglobulin domain; Alternative splicing; Signal.
SIGNAL
CHAIN 20 1092 NEURAL CELL ADHESION MOLECULE 2, 180 kDa
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 PROBABLE

82 N-LINKED (GLCNAC...) (POTENT

219 N-LINKED (GLCNAC...) (POTENT

310 N-LINKED (GLCNAC...) (POTENT

341 N-LINKED (GLCNAC...) (POTENT

417 N-LINKED (GLCNAC...) (POTENT

472 N-LINKED (GLCNAC...) (POTENT

472 N-LINKED (GLCNAC...) (POTENT

472 N-LINKED (GLCNAC...) (POTENT

472 N-LINKED (GLCNAC...) (POTENT

473 N-LINKED (GLCNAC...) (POTENT

474 N-LINKED (GLCNAC...) (POTENT

475 N-LINKED (GLCNAC...) (POTENT

476 N-LINKED (GLCNAC...) (POTENT

477 N-LINKED (GLCNAC...) (POTENT

477 N-LINKED (GLCNAC...) (POTENT)
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EXTRACELLULAR (POTENTIAL)
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PROBABLE.
PROBABLE.
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                                                            EMBL; M76710; AAA49910.1; -.
PIR; JN0635; JN0635.
HSSP; P56276; ITLK.
InterPro; IPR008957; FW_III-like.
InterPro; IPR003961; FW_III.
InterPro; IPR007110; Ig-like.
InterPro; IPR007598; Ig-22.
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59; Conservative 3
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Matches 59; Conserv
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SEQUENCE
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Q91664 xenopus lae Q92d5 mms musculu Q9jka5 mms musculu Q9jka5 mus musculu Q9jka7 homo sapien Q9cva4 mus musculu Q9va4 pallus gall Q9ra42 homo sapien Q9fq7 homo sapien Q9fq7 homo sapien Q9fq8 pallus gall Q9f65 xenopus lae Q86xX7 homo sapien Q7zq1 homo sapien Q7zq1 homo sapien Q9dq4 mus musculu Q9qwm Drachydanio Q8dj27 brachydanio Q8dj27 brachydanio Q801m2 brachydanio Q80490 brachydanio Q90490 brachydanio Q9cwd9 mus musculu Q80713 homo sapien Q80741 brachydanio Q80741 brachydanio Q9cwd9 mus musculu Q80713 homo sapien Q80713 mus musculu

091664 0922DS 0922DS 0922DS 095791 0997WR4 098742 095109 097GPI 097GPI 097GPI 097GPI 090744 090744 090173 0907713 0907713

257 246.5 246.5 219 213 213 213 213 208 197 197 197 198.5 1185.5 1185.5 1185.5 1185.5 1185.5 1187.5 1177.5

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318 319 319 319 319 327 332 332 332 34 35 375 375

407 248 248 1409 11409 11428 358 725 838 838 1181 1181 1031

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June 15, 2004, 10:58:19; Search time 36 Seconds (without alignments) 2716.962 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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AL IGNMENTS

	"Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular Family?";  Curr. Top. Microbiol. Immunol. 251:91-98 (2000).  [2]  SEGURENCE FROM N.A.  STRAIN-C57BL/67; TISSUE-Embryo;  KRANIN-C57BL/67; TISSUE-Embryo;  Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Salto R.,  KANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN-CANIN
	Schriml L.M., Staubli F., Sızuki R., Tomita M., Magner L., Washio T Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Bustindich S., Hill D., Hoffmann M., Hume D.A., Kaniya M., Lee N.H., Lyone P., Marchionni L., Machima J., Mazzaralli J., Mombaerte P.,
RA Lyon	Ivons P. Marchionni L. Mashima J. Mazzarelli J. Mombaerts P.

Q9epk4 mus musculu Q9dBb7 mms musculu Q9dBb7 mms musculu Q9bx67 homo sapien Q9fE11 homo sapien Q9fE11 homo sapien Q9fE11 homo sapien Q9fE1 homo sapien Q9fE29 mus musculu Q8c59 mus musculu Q7xwt0 xenopus lae Q7syf7 xenopus lae Q9y5b2 homo sapien Q8bx59 mus musculu Q7syf7 xenopus lae Q9by5b2 homo sapien Q8bx59 mus musculu Q9jkd5 rattus norv

Q9EPK4 Q9D18B7 Q9D18B7 Q96W1L8 Q96FL1 Q97159 Q97159 Q97159 Q72W71 Q972B2 Q72W71 Q972B2 Q72W71 Q972B2 Q972B2

1615 1604 1604 1409 1400 1400 1400 494.5 494.5 454 456 456 469.5 469.5 470 3340 3340 331

Description

us-09-524-531c-13.rspt

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Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Mesonephros;
MEDLINES-223546B1; PubMed=12466B51;
The PANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; R., Rawaji H., Kohtsuki S., *Punctional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MALSRRIRLRLYARLPDFFILLTLFRGCMI EAVNLKSSNRNPVVHBFESVELSCIITDSQT
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JCAM3 OR JCAM2 OR 1110002N23RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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98.9%; Score 1615; DB 11; Length 310;
Best Local Similarity 99.4%; Pred. No. 1.1e-152;
Matches 308; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                    Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00408; ĬĠc2; 1.
PROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domaiñ; SEQUENCS 310 AA; 34837 MW; 4B92BCB51D0A4B0A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1933825; Jam3.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                SEQUENCE PROM N.A.
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                                                                                                                                                                                         TISSUE=Kidney;
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SEQUENCE FROM N.A.

STRAIN=CSTRIN_60; TISSUB-Small intestine;

KAMAIN=CSTRIN_60; TISSUB-Small intestine;

KAMAIN=CSTRIN_60; TISSUB-Small intestine;

KAMAIN_1. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Pukumishi Y., Konno H., Adachi J., Pukuda S.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,

Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Suzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,

Nymachia-P., V.,

Wanshia-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nymachia-P., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDPRIEWKKIQDGGTTYVYFDNKIGGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(KSI_TaxID=10090;
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InterPro; IPR007110; Ig-like.
InterPro; IPR007598; Ig_c2.
Ffam; PR00047; 1g; 2.
SWART; SW00408; IGc2; 1.
EROSITE; PSS0835; IG_LIKE; 2.
Immunoglobulin domain and an 34855 MW; C74884EABE234680 CRC64;
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09D1M9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
1110002N22Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
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98.7%; Pred. No. 1.4e-151;
rative 1; Mismatches 3;
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Best Local Similarity 98.79
Matches 306; Conservative
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                                                                                                                                                  C STRAINC57BL/65; TISSUB=Embryo;

K MEDLINE=2108566; PubMed=11217851;

K RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Haraw A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Harawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golbori T., Bono H., Kasukawa T., Saito R., Ashburner M., Batalov S., Casawant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Rabil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinthaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S., Nasachi Y., Kawashi Y.
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Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 1.8e-151;
2; Mismatches 3; Indels 0
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PROSTIE; PS:00835; IG LIKE; 2.
Immunoglobulin domain.
SEQUENCE 310 AA; 34819 MW; 6692BCAD68EA4BID CRC64;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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Best Local Similarity 98.4%;
Matches 305; Conservative
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|DFKHKIAFVI 310
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                                                                               NCBI_TaxID=10090;
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Q9BX67; Q9BX67; 01-JUN-2001 01-JUN-2001 01-OCT-2003

PRELIMINARY;

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181 PTDSRANPRFONSSFHVNSETGTLVFNAVHGDDSGQYYCIASNDAGAARCBGQDMBVYDL 240
181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMBVYDL 240
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Junctional adhesion molecule 3 precursor (Junctional adhesion molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein FLJ90288) (Hypothetical protein FLJ90888).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L., "Heterogeneity of endothelial junctions is reflected by differential expression and specific subcellular localization of the three JAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoro J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Yamamoro J., Wakamatsu R., Yakamura Y., Kojima S., Nagahari K., Hattori A., Okumura K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF356518; AAXZ72211; --

EMBL, AJ344431; CAC69845.1; --
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                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
"Characterization of Junctional Adhesional Molecule-3 on Human Platelets: A New Member of Immunoglobulin Superfamily.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.3%; Score 1409; DB 4; Length 310; Best Local Similarity 85.8%; Pred. No. 4.2e-132; Matches 266; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H. "Junctional adhesion molecules (JAMs) and interendothelial
                                                                                                                                                                                                                                                                                                                                                                      Cunningham S.A., Arrate M.P., Tran T.M.; "Cloning of Human Junctional Adhesion Molecule 3."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                              Homo sapiens (Human).
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46 MALRRPPRIRICARLPDFFILLLFRGCLIGAVNLKSSNRTPVVQRFESVELSCIITDSQT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Phillips H.M.;
"Narrowing the critical region within 11q24-qter for hypoplastic left heart and identification of a candidate gene, JAM3, expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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86.3%; Score 1409; DB 4; Length 355;
Best Local Similarity 85.8%; Pred. No. 5e-132;
Matches 266; Conservative 18; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 76 355 JUNCTION ADHESION MOLECULE 3. SEQUENCE 355 AA; 39602 MW, 8B1577DEA7BID4F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hearn T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiogenesis.";
Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AJ416101; CAC94776.1; -.
Genew, HGNC.1.5532; JAM3.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                355 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Junction adhesion molecule 3.
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SMART; SM00408; 1Gc2; 1.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                      DFRHKSSFVI 310
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10 QBWATB
10 QBWATB
10 QBWATB
10 QBWATB
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11 QBWATB
12 QBWATB
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14 QBWATB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DPRIEWKKIQDEGTTYVPPDNKIGGDLAGRAEILGKTSLKIWNYTRDSALYRCEVVARN 120
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular endothelial junction-associated molecule (Junctional adhesion molecule-3) (2410030G21Rik protein).
03AM2 OR JCAM2 OR JCAM2 OR JAM-3 OR 2410030G21RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALREPELRICARLEDPFLILLFRGCLIGAVNLKSSNRTPVVQBFBSVELSCIITDSQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TDSRANPRFRNSGFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 IAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGRSYKSPGKHDGVNYIRTSEBGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ALSRRIRLRLYARLPHFFILLLFRGCMIRAVNIKSSNRNPVVHEFRSVELSCIITHSQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 IDSRANPRPQNSSPHVNSBTGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLN
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                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 309;
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                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC010690; AAH10690.1; -
InterPro: IPR007510; Ig-11ke.
InterPro: IPR007598; Ig-c2.
Pfam; PP00047; Ig-2.
SWART; SM00408; IGc2; 1.
SROSTER; PS50835; IG_LIKE; 2.
HyporINE; PS50835; IG_LIKE; 2.
NON_IER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA.
PRT;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Eye;
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SEGUENCE FROM N.A.
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KRAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Pukumishi Y., Komono H., Adachi J., Pukuda S.,

RA Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Patuli Y., Golobori T., Bano H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Baldarelli R.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,

RA Sakai K., Okido T., Fletcher C., Fullita M., Gariboldi M.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Nurahaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Punctional annotation of a full-length mouse cDNA collection.",

Nurahara Annotation A., Mang K., Wawaji H., Kohtsuki S.,

Ratter 4095-865-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 SLLGNPKGGTHNNSSYTWYTKSGILQFNMISKYDSGEYYCEARNSVGHRRCPGKRMQVDV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 RIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                 Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.; "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RLEWKKVGGG-VSLVYYQQALQGDFKDRAEMI-DPNIRIKNVTRSDAGBYRCEVSAPTEQ
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                        MEDLINE=20317114; PubMed=10779521;
Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
Vascular Endothelial Junction-associated Molecule, a Novel Member
the Immunoglobulin Superfamily, Is Localized to Intercellular
Boundaries of Endothelial Cells.";
J. Biol. Chem. 275:19139-19145 (2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Mismatches 115; Indels
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EMBL, AA291757; CAC26699.1; -.
EMBL, AK013914; BAB29053.1; -.
EMBL, AK010616; BAB27064.1; -.
MCD, MCI:1933820; Jam2.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 116; Conservative
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                                                                                                                                                                                                                                                               PubMed=11036763;
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                                                                                                                                                                                                                                      SEQUENCE
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RIEWKKIODGQTTYVYPDNKIQGDLAGRIDVFGKTSLRIWNVTRSDSAIYRCEVVALNDR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 DSRANPR----FQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 INISGIIATVVVVARVISVCGLGTCYAQRKGYP--SKRTSPQKGSP-----ASKVTTMSE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
EMBL; AK020157; BAC20102.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 -KEVDBITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQBSBGYPRPHYSWYRNDVPLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ARLPHFFLILLFRGCMIRAVNLKSSN-----RNPVVHEFESVELSCIITHSOTSDP
                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.3%; Score 494.5; DB 11; Length Best Local Similarity 37.0%; Pred. No. 8.4e-41; Matches 115; Conservative 54; Mismatches 115; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB8227EC13D349A3 CRC64;
                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TYBALNA-CSTBL/66; TISSUE-SKin,
MEDILINE-22354683; PubMed=12466851;
The PANTOM COMBOTTIUM,
                                                                                                                                                                                                                                                                                    Junction cell adhesion molecule 2. JAM2 OR JCAM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE, PS50835; IG LIKE; 2.
SEQUENCE 298 AA; 33079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig c2.
InterPro; IPR003596; Ig v.
||:| ||:|
NDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00047; 19; 2.
SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                 PRELIMINARY;
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288 NDFKHTKSFII 298
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                 Q8CB95
                                                                                                           RESULT 8
QBCR95
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QBC5K9
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GONLOBDKVMLEVIJVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYTWFKDGHSL-- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSRANPR---PQNSSPHVNSETGTLVPNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LGNPKGRTHNNSSYTMNTKSGILQPNMISKMDSGBYYCRARNSVGHRRCPGKRMQVDV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ARLPHPFLLLLPRGCMIEAVNLKSSN------RNPVVHEPESVELSCIITHSQTSDP 63
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                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=223546B3; PubMed=12466B31;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AR07812B; BAC37139.1; -.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NDBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%; Score 494.5; DB 11; Length 298; 37.3%; Pred. No. 8.4e-41; Live 53; Mismatches 115; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00047; 19; 2.
SWART; SM00409; IG; 2.
SWART; SM00408; IGc2; 2.
SWART; SM00408; IGc2; 2.
SWART; SM00408; IGv; 1.
PROSITE; PSS0835; IGv; 1.
SRQUENCE 298 AA; 33182 MW; 1131F0BFDB9CEB51 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                          , Last annotation update)
  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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                     01-OCT-2003 (TrEMBLrel. 25, Last an
Junction cell adhesion molecule 2.
                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1933820; Jam2.
InterPro; IPR003599; IG.
InterPro; IPR00710; IG-like.
InterPro; IPR003598; IG-2.
InterPro; IPR003596; IG-V.
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288 NDPKHTKSPII 298
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                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                  JAM2 OR JCAM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVLAVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRIS--BEGDPRHKSSPVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 LILLGLLIFGIWPAYSRGYFERTKKG---TAPGKK--VIYSQPSARSEGBFKQTSSFLV 300
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the RIKEN Genome Exploration Research Group Phase I & II Team;
#Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas.";
Nature 420:563-573(2002).
BEMBL; AR031574; AAL21876.1;
EMBL; AR031574; BAC28369.1;
MGD; MGI:1321398; FILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 LLLLPRGCMI-EAVNLKSSNRNP----VVHEFESVELSCIITHSQTSDPRIEWKKIQDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 TTYVYPDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVALNDRKGVDBITIELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 VQVKPVTPVCRIPAAVPVGKTATLQCQBSBGYPRPHYSWYRNDVPLPT-DSRANPRPQNS
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                      27.6%; Score 450.5; DB 11; Length 300; 38.0%; Pred. No. 2.1e-36; ive 52; Mismatches 115; Indels 19;
STRAIN=Sprague Dawley;
Mashima H., Kojima I.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Junction cell adhesion molecule)
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                              EMBL; AF276998; AAF78250.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 300 AA; 32369 NW; 45AE362A96159BFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005515; P:protein binding; IPI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; T1SSUB=Cecum;
MEDLINE=22354683; PubMed=12466851;
The PANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 38.04
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
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TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Rightsersoft, Standard E.A., Grouse L.H., Derge J.G.,
Rightsers R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Rightser R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh P.,
Distchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B. Donaldo M.F., Casavant T.L., Scheetz T.E.,
Recharstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rochards S.M., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,
Rahey J., Helton B., Ketteman M., Maddan A., Youffeus S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rahetiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Lenger R.D., Willer L.D., Myers R.M., Butterfield Y.S.,
R. Generation and intitial analysis of more than 15,000 full-length human
190 VLKFAAVSTSDSGEYYCEATWNQGKQASDLVRMDVQDVNVGGIVAAVVIVLLILALIGFG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 VKGGDSPDLRC----SYTSDYINPRVENKPVNKDQETSFVFYDGSLTASYKDRATSYPQ- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 SLRIWNVTRSDSAIYRCEVVALNDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 VHEFESVELSCIITHSQTSD---PRIEWKKI-QDGQTTYVYFDNKIQGDLAGRIDVFGKT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Bukaryota; African clawed frog).
Bukaryota; African clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 300;
                                                                                                  263 ICCAYRRGCFISSKQDGBSYKSPGKHDGVNYIRTSREGDFRHKSSFVI 310
                                                                                                                                      55; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIŠSUR=Whole;
Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO54305; AAH54305.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 AA; 32858 MW; 02BC49DC74E271D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 409.5; DB 1
Pred. No. 2.6e-32;
                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiative
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                                                                                                                                                                                                                                                                                                                          07SY07
                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                           SO TENER REPRESENTE TO THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                               | | | :::: | | | | ::: | | | | ::| | TALVCYNSQITAPYADRV-TPSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAA-RCEGQDMEVYDLNIAGIIGGVLVV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 KIQGDLAGRIDVPGKTSLRIWNVTRSDSALYRCEVVALNDRKEVDBITIBLIVQVKPVTP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 VCRIPAAVPVGKTATLĄCQESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSFHVNSETG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 TLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDLNIAGIIGGVLVVLIVLAVITMG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                  LIVLAVITMGICCAYRRGCPISSKQDGESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOVKPVTPVCRIPAAVPVGKTATLOCOBSEGYPRPHYSWYRNDVPLPT-DSRANPRFONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 CMIEAVNLKS-SNRNP---VVHEPESVELSCIITHSQTSDPRIEWKKI-QDGQTTYVYFDN
                                                                                                                                                                                                                                  20 LILLFRGCMIRAV-----NLKSSNRNPVVHEFESVELSCIITHSQTSDPRIEWKKIQDGQ
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to junctional adhesion molecule 1.
Stenpus laevis (African clawed frog).
Bukaryot laevis (African Clawed frog).
Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                   15;
                                                                                                        DB 11; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 289;
                                                                                                        27.4%; Score 447.5; DB 11; Length 34.2%; Pred. No. 4.2e-36; tive 63; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 289 AA; 31630 MM; 24354B5A37619845 CRC64;
             Hypothetical protein.
SEQUENCE 300 AA; 32423 MW; 3CE561E8FF3B97EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.1%; Score 426; DB 13; 34.0%; Pred. No. 5.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
InterPro, IPR003598; Ig_C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                      Best_Local Similarity 34.2<sup>3</sup>
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Conservative
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SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
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                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 GIKLNOVTRKDAGEYSCEVTSTGTKVLYGRAKIQLQVIVAPGTPVAQVPSSARTGSVABL 162
                                         163 MCVETQGPPLPTFYTHYRHNSPMQAKS-----QNSTYTIDPNTGVLKFASVGTSDSGEYY 216
                                                                   CIASNDAGAARCEGODMEVYDLAIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKOD 278
                                                                             42 VVHEFESVELSCIITHSQTSDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 IWNVTRSDSAIYRCEVVALNDRKEVDBITIBLIVQVKPVTPVCRIPAAVPVGKTATLQCQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESEGYPRPHYSWYRNDVPLPTDSRANPRPQNSSPHVNSETGTLVFNAVHXDDSGQYYCIA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNDAGAARCEGO-DMEVYDLAIAGIIGGVLVVLIVLAVITMGICCAYRRGCPISSKQDGB 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 QCQESEGYPRPHYSWYRNDVPLPTDSRANPRFQNSSPHVNSETGTLVPNAVHKDDSGQYY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 ILPENNPVKLSC--AYSGFSSPRA------ASYEDRV----TFLPTGIT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%; Score 340; DB 4; Length 259;
30.9%; Pred. No. 1.9e-25;
tive 48; Mismatches 106; Indels 34;
                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                           279 GESYKSPGKHDGVNYIRTSEEGDFRHKSSFVI 310
                                                                                                                       277 KVIYSQPSE------TRSDKNFQQTSSFLV 300
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                                                                                                                                                                                                                                  Junction adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 30.99
nes 84; Conservative
                                                                                                                                                                                 PRELIMINARY;
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64 AA

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                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
RMBL; AK017692; BAC25526.1; -.
NON TER 1 1 1
SEQÜENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GGVLVVLIVLAVITMGICCAYRRGCPISSKQDGBSYKSPGKHDGVNYIRTSBEGDFRHKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGVLVVLIVLAVITWGICCAYRRGCFISSKQDGBSYKSPGKHDGVNYIRTSBEGDFRHKS
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                                                                                      Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.6%; Score 336; DB 11; Length 64; 100.0%; Pred. No. 7.1e-26; rive 0; Mismatches 0; Indels
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Junction cell adhesion molecule 3 (Fragment).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TYRAIN-E/STBL/60; TISSURE-BOdy;
MEDLINE-22354683; PubMed-12466851;
The PANTOM CONSORTIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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SFVI 64
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26         310         100.0         310         6         ABA57309         Ada57309         Ada57309 Human sec           27         310         100.0         310         6         ABU71277         Abu81127         Abu81127	ALI GNMENTS	AAY96735 ID AAY96735 standard; protein; 310 AA.	Notified-site   10cation/Qualifiers   10cation/Qualifiers   1.30
otein - proton:  July and a sore:  Ince:  Ing table:  Ched:  Thed:	Word Bize : 0 Total number of hits satisfying chosen parameters: 1586107	DB seq length: 0 DB seq length: 2000000000 cessing: Listing first 45	   Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.    Core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Human PRO1868 protein UNQ859 SEQ ID NO:193
AAB33457 standard; protein; 310 AA
                                                 (first entry)
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02-JUN-1999;
23-JUN-1999;
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05-OCT-1999;
29-OCT-1999;
29-NOV-1999;
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01-SEP-1999;
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13-SEP-1999;
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04-MAY-1999
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                        AAB33457;
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                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encodes a PRO polypeptide which is
                                                                                                                                                                                                                        Perrara N, Fong S, Gao W, Goddard Stewart TA, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 310; DB 3; Length 310; Best Local Similarity 100.0%; Pred. No. 1.6e-295; Matches 310; Conservative 0; Mismatches 0; Indels
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                                                            980S-0113145P.
980S-0113511P.
990S-0115558P.
990S-0115565P.
                          99WO-US02B634
                                                  98US-0112851P.
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Pan J, Roy MA,
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                                                                                                                                                                                                                                                                                                                                transmembrane polypeptide.
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N-PSDB; AAA51265.
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                                                 16-DEC-1998;7
16-DEC-1998;7
22-DEC-1998;
                          01-DEC-1999;
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 22-JUN-2000
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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antiarthritic; antirheumatic; immunosuppressive; where most antiansemic; hepatotropic; virucide; antipooriatic; antialergic; antiansemic; hepatotropic; virucide; antipooriatic; antialergic; antiaschmatic; systemic lupus erythematosus; rheumatoid arthritis; sondyloarthropathy; systemic sclerosis; sarcoidosis; widiopathic inflammatory myopathy; systemic sclerosis; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; wutoimmune thrombocytopaemia; immune-mediated renal disease; democytopaemia; immune-mediated fenal disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; munnological disease; transplantation associated disease; transplantation associated disease;
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990S-0123957P.
990S-0125775P.
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99US-0131445P.
99US-0132371P.
99US-0134287P.
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2000WO-US000277.
2000WO-US000376.
2000WO-US003565.
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99WO-US028301
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99WO-US028551
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99WO-US028565
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(GETH ) GENENTECH INC.

RESULT 2

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24-APR-2001 (first entry)
                                                                 Homo sapiens
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                                                                                                                                                               The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodise, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33477 represent human PRO perseent invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                      Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 Henzel W;
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Gurney AL, Hebert C, Hi, Shelton DL, Smith V; Nood WI, Yan M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 310; DB 3; L
100.0%; Pred. No. 1.6e-295;
tive 0; Mismatches 0;
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                           Wood WI,
P, Goddard A,
an J, Pennica D
Watanabe CK, W
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                                                                                                                                            Claim 33; Fig 88; 309pp; English
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Ashkenazi AJ, Baker KP,
Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
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nes 310; Conservative
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                                                   2000-572271/53.
                                                   WPI; 2000-572271/
N-PSDB; AAC58622.
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181 PTDSRANPRENSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NDRKBIDBIVIBLTVQVKPVTPVCRVPKAVPVGKMATLHCQBSEGHPRPHYSWYRNDVPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MALREPPELATICARLEDFFILLTFRGCLIGAVNAKSSNRTFVVQFFSSVELSCIITDSOT
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Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule; inflammation; cancer; wound; angiogenesis; human; confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
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100.0%; Score 310; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 6; 59pp; English
                                                                                                                                                                                                                                                                                                13-MAR-2000; 2000WO-EP002219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imhof BA, Aurrand-Lions M;
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N-PSDB; AAA95306.
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transmembrane
                                            antiinflammatory;
                                                           antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant; antiangiogenic; vasotropic; antiathmatic; antirheumatic; cancer; antiantiantic; antiantertility; antidiabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y one nucleic acids encoding PRO polypeptides which are useful in thu tment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of sixty one novel secreted and transmembram diseases (e.g. The RD polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodeganerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. enterocolitis), neurodeganerative ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), inflammatory infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara N;
(B, Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J, Botstein D, Desnoyers L, Baton DL, Ferrara N; Pong S, Gao W, Gerber H, Gerritsen MB, Goddard, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ; Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D; Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 310; DB 4; Length 310; 100.0%; Pred. No. 1.6e-295;
                                          Human; PRO; dermatological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 124; 393pp; English.
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99WO-US023089.
99WO-US028214.
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99WO-US028565.
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99WO-US021090
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2000WO-US000219
                                                                                                                        ischaemia; inflammation.
              Human PRO1868 protein.
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N-PSDB; AAP72433.
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Mather JP, Pa
Williams PM,
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Filvaroff E,
                                                                                                                                                       Homo sapiens
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02-DEC-1999;
02-DEC-1999;
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15-SEP-1999
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29-NOV-1999
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disease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length methods the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from BPO
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SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNYTRDSALYRCEVVAR
                                                                                                             SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR
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Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; full length cDNA; cDNA synthesis; oligo-capping
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K, Kojima S, Otsuk
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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N-PSDB; AAK94867.
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for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primars enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                                                                                                                                                Length 310;
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Best Local Similarity 100.0%; Pred. No. 1.6e-295;
Matches 310; Conservative 0; Mismatches 0;
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99WO-USO28634.
99WO-USO28551.
99WO-USO28564.
99US-0170262P.
99WO-USO30995.
99WO-USO309911.
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02-DEC-1999;
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16-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O Primers useful for synthesizing full length cDNA clones and their use genetic manipulation.
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                                                                                                             Gape
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T, Koga
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                                                                 Length 310;
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                                                                                                          Indels
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S, Otsuki
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                                                                 'Match 100.0%; Score 310; DB 4; L
Local Similarity 100.0%; Pred. No. 1.6e-295;
les 310; Conservative 0; Mismatches 0;
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K, Kojima S
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2000JP-00118774.
2000JP-00183765.
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N-PSDB; AAK94243.
                            Sequence 310 AA;
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02-MAY-2000;
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ANUIS172-AAU1246 represent novel human secretory and transmembrane PRO CC polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides. To nothink bioactive molecules to calls expressing PRO CC polypeptides, to link bioactive molecules to calls expressing PRO CC polypeptides, to modulate biological activities of cells expressing PRO CC polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a call sample to that in a control sample. Some CC of the 275 sequences are also useful to stimulate the release of tumour confiferation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the release of control of proteoglycans from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells or of T-configurations of propeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used in assays to identify molecules convolved in pinding and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000WO-US005819.
15-MAR-2000; 2000WO-US006819.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
21-MAR-2000; 2000WO-US00732.
30-MAR-2000; 2000WO-US007832.
30-MAR-2000; 2000WO-US013705.
17-MAY-2000; 2000WO-US013705.
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02-UUN-2000; 2000WO-US015564.
05-UUN-2000; 2000WO-US012504.
28-UUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
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24-AUG-2000; 2000MO-US023328.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum:
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N-PSDB; AAS21512.
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11-PEB-2000; 2
18-PEB-2000; 2
22-PEB-2000; 2
24-PEB-2000; 2
24-PEB-2000; 2
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100.0%; Score 310; DB 4; Length 310; 100.0%; Pred. No. 1.6e-295;
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                          0; Mismatches
               Best Local Similarity 100.
Matches 310, Conservative
  Query Match
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Sequence 310 AA;

preparations

The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiova arrest, cerebrovascular disorders e.g. carebrovassular e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food

Claim 11; Page 538-539; 601pp; English.

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SDPRIEWKKIQDEGTTYVPFDNKIQGDLAGRAEILGKTSLKIWNYTREDSALYRCEVVAR 120
                                          SDPRIEWKKIODBQTTYVFPDNKIQGDLAGRABILGKTSLKIWNYTRRDSALYRCEVVAR 120
                                                                                       NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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           1 MALRRPRIALCARLPDFFILLLFRGCLIGAVNLKSSNRTFVVQFFESVELSCIITDSQT
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MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFESVELSCIITDSQT
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Komatsoulis GA;
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Birse CE,
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Olsen HS,
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Lafleur DW,
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                                                                                                      protein; human; autoimmune; hyperproliferation; cardiovascular;
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Komatsoulis GA;
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100.0%; Score 310; DB 4; L 100.0%; Pred. No. 1.6e-295;
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Olsen HS,
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310; Conserv
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                      Best Loca
Matches
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The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardioc arrest, cerebrovascular disorders e.g. cerebronia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food

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                                                                                                                                                                       SDPRIEWTKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNYTRNDSALYRCEVVAR
                                                                                                                                                                                                                                   NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                                                                                                             241 HIGGIIGGVLVVLAVLALITIGICCAYRRGYFINNRODGESYRNPGKPDGVNYIRTDEEG
                                                                                                                                                       SDPRIEWKKI QDEQTTYVPPDNKI QGDLAGRABI LGKTSLKI WNVTRRDSAL YRCEVVAR
                                                                                                                                                                                                                 NDRKBIDBIVIBLTVQVKPVTPVCRVPKAVPVGKMATLHCQBSBGHPRPHYSWYRNDVPL
                                                                                                                                                                                                                                                                             PTDSRANPRPRNSSPHENSBTGTLVPTAVHKDDSGQYYCIASNDAGSARCBQEMBVYDL
                                                                                                                                                                                                                                                                                               18.1 PTDSRANPRFRNSSPHLNSBTGTLVFTAVHXDDSGQYYCIASNDAGSARCBEQEMEVYDL
                                                                                                                                                                                                                                                                                                                                           NIGGIIGGVLVVLAVLALITLGICCAYRRGYPINNKQDGBSYKNPGKPDGVNYIRTDEBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA;
                                                                                          MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT
                                                                                                                        MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFBSVBLSCIITDSQT
                                                            Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding 29 secreted proteins, for diagno preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism
                                                            ö
                             Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ni J, Soppet DR,
Komatsoulis GA;
                                                            Indela
                             Score 310; DB 4; I
Pred. No. 1.6e-295;
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                                                          0; Mismatches
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Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11, Page 559-560; 601pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein encoded by gene #39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB80409 standard; protein; 310
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Olsen HS,
                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2000; 2000WO-US019735.
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                         Query Match
Best Local Similarity 100.
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       DPRHKSSPVI 310
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                                                                                                                                                                                                                                                                                                                                                                                                                       Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-123261/13
Sequence 310 AA;
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liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral isohemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Also used in food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927; inflammatory disorder; immune related disease; rheumatoid arthritis; systemic lupus erythematosus; systemic sclerosis; thyroiditis; autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
                                                                                                                                                                                     1 MALRRPPRIRICARLPDFFLLILFRGCLIGAVNIKSSNRTPVVQEPESVELSCIITDSQT
                                                                                                                                                                                                                              SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted and transmembrane protein; PRO1800; PRO539; PRO982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune haemolytic anaemia, diabetes mellitus, infectious hepati
psoriasis, allergic disease of the lung, graft-versus host disease,
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                                                                                                               Length 310;
                                                                                                                                         Indels
                                                                                                              Score 310; DB 4; L; Pred. No. 1.6e-295; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG92709 standard; protein; 310
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98US-0113145F,
98US-0113511F,
99US-011558F,
99US-0115565F,
99US-0115733F,
99US-011934F,
99US-0119965F,
                                                                                                              100.0%;
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                                                                                                                                      Matches 310; Conservative
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                                                                                                            Query Match
Best Local Similarity
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                                                                                   Sequence 310 AA;
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                                                          preparations
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10-FEB-1999;
12-FEB-1999;
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16-DBC-1998;
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22-DEC-1998;
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12-JAN-1999;
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mainto acid sequence identify to secreted and transmembrane polypeptides PRO180, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO334 or PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or PRO18015, and their encoding mucleic acids. Also included are vectors, host cells and antibodies against PRO polypeptides. PRO proteins are useful for identifying modulators of the polypeptide. PRO1868 useful for the dagnosis and treatment of inflammatory and immune related diseases in including systemic lupus erythematosus, rheumatoid arthritis, systemic solvensis, autoimmune haemolytic amemia, thyroiditis, diabetes mellitus, infectious hepatitis, psoriasis, allergic diseases of the lung and graft-versus host disease and tumours. Pro nucleic acids are useful for constructing hybridisation probes for mapping the gene that encodes that PRO and for the genetic analysis of individuals with genetic disorders, and for generaling transgenic animals which are useful in the development and screening of therapeutically useful reagents. PRO nucleic acids are also useful for gene therapy, chromosome identification, and tissue constructions purposes. The anti-PRO antibodies are useful in electrophoresis purposes. The anti-PRO antibodies are useful in clectrophoresis purposes. The anti-PRO protein service for affinity purification of PRO. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated polypeptide having at least 80%
                                                                                                                                                                                                                                                                                                                         W, Goddard A;
Watanabe CK;
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                                                                                                                                                                                                                                                                                                                         Perrara N, Fo
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                                                                                                                                                2000US-0187202P.
2000WO-US008439.
2000WO-US014941.
2000WO-US015264.
                99US-0162506P.
99WO-US028634.
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99US-0170262P.
2000WO-US003565.
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an J, Roy MA,
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                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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N-PSDB; ABS68392.
                                                                                                                                                                                                                                                                                                                                                Pan J,
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                29-OCT-1999;
01-DBC-1999;
02-DBC-1999;
09-DBC-1999;
11-FEB-2000;
22-FEB-2000;
02-MAR-2000;
30-MAR-2000;
30-MAR-2000;
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02-JUN-2000;
01-DEC-2000;
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Wood WI;
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administered therapeutically, especially by expressing encoding
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                                                                                                                                                                                                                                                Sequence 310 AA;
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                                    241 NIGGIIGGVLVVIAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEBG 300
                                                                                                                                                                                                                                                                                                                                                       secreted protein; transmembrane protein; gene mapping; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to new human secreted and transmembrane proteins (PRO) and mucleic acids of the invention. The polypeptides can be
                    NIGGIIGGULVVLAVLALITLGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDEEG
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Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human secreted and transmembrane (PRO) polypeptides, useful for treating conditions requiring PRO polypeptides, for screening PRO antagonists and agonists useful as drug candidates.
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, Stewart TA,
                                                                                                                                                                                                               ABG91361 standard; protein; 310 AA.
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                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #7.
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990S-0115565P.
990S-0115733P.
990S-0119341P.
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99US-0162506P.
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30-MAR-2000; 2000WO-US008439.
30-MAY-2000; 2000WO-US014941.
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Pan J, Roy MA,
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02-JUN-1999;
29-CCT-1999;
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02-DEC-1999;
11-FBB-2000;
22-FBB-2000;
22-FBB-2000;
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Gurney AL, 1
Wood WI;
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polynucleotides, e.g. in therapeutic compositions. They can be used to polynucleotides, e.g. in therapeutic compositions. They can be used to dereen for PRO polypeptide antagonists and agonists useful to identify drug candidates. They can also be used to produce antibodies, useful to detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or therapeutically (e.g. as antagonists or to target and/or deliver cyctoxic agents). The polynucleotides are useful therapeutically e.g. to produce antisense sequences to inhibit polypeptide production. They can be used to produce probes and primers useful to detect or isolate sequences encoding PRO polypeptides or similar sequences e.g. variants or sequences from other species. They are also useful for gene mapping and to generate transgenic animals. ABG91355-ABG91363 represent human PRO
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1 MALRRPPRIRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVOBFESVELSCIITDSOT

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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antianglogenic, hypotenaive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping, ABL88259 to ABL88257 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00816744.
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2001US-00796498.
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                        25-JJL-2000;
28-JJL-2000;
02-AUG-2000;
17-AUG-2000;
24-AUG-2000;
24-AUG-2000;
07-SEP-2000;
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08-NOV-2000;
10-NOV-2000;
01-DEC-2000;
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20-DEC-2000;
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Paoni NF;

0; Gaps 100.0%; Score 310; DB 5; Length 310; 100.0%; Pred. No. 1.6e-295; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 310; Conservative Query Match

241 NIGGIIGGYLVVLAVLALITIGICCAYRGYPINNRQDGBSYRNPGRPDGVNYIRTDEBG 300 241 NIGGIIGGYLVVLAVLALITIGICCAYRRGYPINNRQDGBSYRNPGRPDGVNYIRTDEBG 300 121 NDRKEIDEIVIELTVQVXEVTPVCRVPKAVPVGKWATIHCQESEGHPRPHYSWYRNDVPL 180 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNYTRDSALYRCEVVAR 120 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATTHCQESEGHPRPHYSWYRNDVPL 180 SDPRIEWKKIQDBQTTVVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEGGEMBVYDL PIDSRANPRFRNSSFHLINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCERQEMEVYDL New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein. Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin, HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; disorder; hammective disorder; conscrive disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; Claim 1; Page 1895; 2102pp; English. Human albumin fusion protein #1972. ABG65297 standard; protein; 310 AA 12-APR-2000; 2000US-0229358P. 25-APR-2000; 2000US-0199384P. 21-DBC-2000; 2000US-0256931P. 12-APR-2001; 2001WO-US011988. (HUMA-) HUMAN GENOME SCI INC. osteopathic; antiarthritic (first entry) Rosen CA, Haseltine WA; DPRHKSSFVI 310 DFRHKSSFVI 310 WPI; 2002-010886/01. WO200177137-A1. sapiens. 27-AUG-2002 18-OCT-2001 Synthetic 61 121 181 ABG65297; 181 301 301 61 Homo RESULT 14 ABG65297 ጵ 셤 Š 셤 ઠે 셤 ð 셤 8 a 

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           immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haemacopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, eningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis) ABG631326-ABG65518 represent albumin fusion proteins of the invention
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                                                                                                                                                                     Gaps
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acquired
                                                                                                                                    Length 310;
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colitis), immune disorders (e.g.
                                                                                                                                      100.0%; Score 310; DB 5; L 100.0%; Pred. No. 1.6e-295;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                    Local Similarity
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, entzfeldt-Jacob disease, encephalomyelitis, meningitis, echizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63126-ABG65518 represent albumin fusion proteins of the invention
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                                                 New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
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                                                                                                    Claim 1; Page 1893-1894; 2102pp; English
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Matches 310; Conservative
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Sequence 423, App
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                                                                             June 15, 2004, 11:08:05 ; Search time 16.5 Seconds (without alignments) 969.942 Million cell updates/sec
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Sequence 190,
Sequence 9, Ap
Sequence 5228,
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Sequence 2778,
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Sequence 2, Ap
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1 MALREPPRIRICARLEDFFL.........VNYIRTDEEGDFRHKSSFVI 310
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-175A-423
US-09-902-175A-423
US-08-1310-912A-190
US-09-301-085-190
US-09-301-300-300-
US-09-134-001C-5228
US-09-134-001C-5228
US-09-134-001C-5228
US-09-134-000C-6778
US-09-252-991A-17237
US-08-252-991A-17237
US-08-444-272-2
US-08-446-200-2
US-08-467-070-2
US-08-467-070-2
US-08-9188-2
US-08-9188-3
US-08-131-237C-5
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                                                     - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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No.
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28		2.3	333	H	JS-08-148-215A-4	sednence	4, Appli
29	۲	2.3	333	4	US-09-170-496D-16	Sequence	16, Appl
30	7	2.3	333	4	US-09-170-496D-172	Sequence	172, App
31	7	2.3	454	4	JS-09-240-639-11	Sequence	11, Appl
32	7	2.3	494	4	US-09-252-991A-28162	Sequence	28162, A
33	7	2.3	503	4	JS-09-215-694-8	Sequence	8, Appli
34	7	2.3	517	•	US-09-252-991A-19322	Sequence	19322, A
35	7	2.3	524	~	US-08-928-692-12	Sequence	12, Appl
36	7	2.3	524	4	US-09-339-972-12	Sequence	12, Appl
37	7	2.3	547	4	US-09-252-991A-18576	Sequence	18576, A
38	-	2.3	256	4	US-09-252-991A-18110	Sequence	18110, A
39	7	2.3	603	4	US-09-252-991A-25264	Sequence	25264, A
40	7	2.3	621	~	US-09-252-991A-19749	Sequence	19749, A
41	7	2.3	642	_	US-08-706-936-2	Sequence	2, Appli
42	7	2.3	642	_	US-08-706-936-3	Sequence	3, Appli
43	٦	2.3	643	~	US-08-616-844-39	Sequence	39, Appl
44	7	2.3	643	~	US-08-599-654-39	Sequence	39, Appl
45	7	2.3	643	<u>-</u> ۳	US-08-944-868A-39	Sequence	39, Appl

## ALIGNMENTS

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61 SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKYSLKIWNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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100.0%; Score 310; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,125A

CURRENT FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-38

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

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PRIOR PILING DATE: 1999-10-05

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PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07
Grimaldi, Christopher J.
                           Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
                                                                                                                                                                                                                      Roy, Margaret Ann
Stewart, Timothy A.
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVBLSCIITDSQT
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                 FRIOR APPLICATION WUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-20
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Patent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
FILING DATE: 1999-09-15
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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Best Local Similarity 100.0
Matches 310; Conservative
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-905-125A-423
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APPLICANT: APPLICANT: APPLICANT:

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61 SDPRIEWKKIQDEGTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTREDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NIGGIIGGULVVLAVLALITLGICCAYRRGYPINNKQDGESYKNPGKPDGVNYIRTDBBG 300
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APPLICANT: Stackawicz, Brian J.
APPLICANT: Stackawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Katagiri, Pumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Win Guo-Liang
TITLE OF INVENTION: RESC GENE PAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PIDSRANPRFRNSSFHLASETGILVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR
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                                      Query Match
100.0%; Score 310; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.4e-279;
Matches 310; Conservative 0; Mismatches 0;
            PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 310
APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 190, Application US/08310912A Patent No. 5981730 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
STATE: MA
COUNTR: MA
ZIF: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALALE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 DPRHKSSFVI 310
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ORGANISM: Homo Sapien
US-09-902-775A-423
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                   300
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                                                                                                             241 NIGGIIGGULVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
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US-09-902-775A-423
US-09-902-775A-423
Facence 423, Application US/09902775A
Facent No. 6686451
GENERAL INFORMATION:
APPLICANT: Geneticch, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betsein, David
AppliCANT: Botseein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Thmas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Eaton, Dan L.
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Ausubal, Frederick M.
APPLICANT: Baskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Branback, Douglass
APPLICANT: Mindrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
ITILE OF INVENTION: RPSZ GENE FAMILY, PRIMERS, PROBES, AND
ITILE OF INVENTION: DETECTION METHODS
ITILE OF INVENTION: DETECTION METHODS
ITILE REPERENCE: 00786/254002
CURRENT APPLICATION NUMBER: 08/310,912
BARLIER APPLICATION NUMBER: 08/310,912
BARLIER PILING DATE: 1994-09-22
BARLIER PILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/310,912A FILING DATE: September 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.3%; Score 7; DB 3;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches
                                                                              PRIOR STRICT STATES SEQUENCED 22, 1227
CLASSIPTCATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCEJ DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-6906
TELEPHONE: (617) 542-6906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 7; DB 2
100.0%; Pred. No. 10;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-301-085-190
; Sequence 190, Application US/09301085
; Patent No. 6262248
                                                                                                                                                                                                                                                                               TELEX: (61./.
TELEX: 100254
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-912A-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 LALITIG 262
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RESULT 6

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GENERAL INFORMATION:
APPLICANT: GAIY L. BRECON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TILE REPREMENTE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
ERQ ID NO 6750
LENGTH: 215
Sequence 14211, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PREJUNIABE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREJUNIABE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 22004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR APPLICATION NUMBER: US 6/117, 747
PRIOR FILING DATE: 1999-01-29
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| Sequence 6778, Application US/09134000C
| Patent No. 6617156
| GENERAL INPORMATION:
| APPLICANT: Lynn Doucette-Stamm et al TITLE OF INFRATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: NUTBERC ACID AND AMINO ACID SEQUENCES RELATING TO
| TITLE OF INVENTION: ENTERCOCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT PAPLICATION NUMBER: US 60/055,778
| PRIOR FILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6812
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 6778
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 148;
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100.0%; Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-328-352-6750
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Patent No. 6380370

GENERAL INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                              OPEVIEW SYSTEM: DOS SOFTWARE: FASESEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/330,330 FILING DATE: 11.-UUN-199 PRIOR APPLICATION DATA: 10.101455 FILING DATE: 12.-UUN-1998 ATTORNEY/AGENT INPORMATION: AMMER: FRASE, PL.D., J.D., Janis K. REGISTRARION NUMBER: 34,819 REFERENCE/DOCKET NUMBER: 05501/032001 TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.3%; Score 7; DB 4;
100.0%; Pred. No. 71;
tive 0; Mismatches
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100.0%; Pred. No. ...
0; Mismatches
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5228
                    225 Franklin Street
                                                                                                                   COUNTRY:
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 52 aming acids
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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                                                         Boston
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US-09-489-039A-14211
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                                                                                 STATE: MA
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APPLICANT: MARC J. SEUDOMONAS
TITLE OF INVENTION:
APPLICANT: MAC J. SEUDOMONAS
TITLE OF INVENTION: ARUGIBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARUGIBIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,708
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: US 60/094,190
RIOR FILING DATE: 1998-07-27
NUMBER: OS 820 ID NOS: 33142
SEQ 1D NO 17237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: BROWNING, Jeffrey
APPLICANT: WARE, CALL
TITLE OF INVENTION: LYMPHOTOXIN-BETA, LYMPHOTOXIN-BETA
TITLE OF INVENTION: LYMPHOTOXIN-BETA, LYMPHOTOXIN-BETA
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: c/o PISH & NEAVE
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2.3%; Score 7; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: PCT/US91/04588
FILING DATE: 27-JUN-1991
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/544,862
FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: c/o FISH & NEAVE
1251 Avenue of the Americas
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REFERENCE/DOCKET NUMBER: B129CIPII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
                                  Sequence 17237, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/222,614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17237
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; Sequence 32267, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; GRNERAL INFORMATION:
    APPLICANT: Marc J. Rubenfield et al.
    APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT PILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32267
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Sequence 24869, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OP INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OP INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBRUCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24969
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0; Indels
                                             Length 220;
                                                                                                0; Indels
                                             Query Match 2.3%; Score 7; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0;
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US-09-252-991A-32267
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                   50 GGIIGGV 56
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US-09-134-000C-6778
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Scoring table:

Word size :

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US-09-906-646-423

US-09-906-700-423

US-09-903-748-423

US-09-901-119-423

US-09-904-119-423

US-09-904-119-423

US-09-904-23-423

US-09-907-744-423

US-09-903-93-423

US-09-903-93-423

US-09-903-93-423

US-09-903-62-423

US-09-903-62-423

US-09-903-62-423

US-09-903-63-423

US-09-905-05-423

US-09-905-05-423

US-09-905-05-423

US-09-905-713-423

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US-09-902-713-423

US-09-902-713-423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 423, Application US/09909320 Patent No. US20020132240A1 GENERAL INFORMATION:
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Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers, Luc
Baton, Dan L.
    -09-909-320-423
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
         June 15, 2004, 11:10:00; Search time 39 Seconds (without alignments) 2239.361 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-907-841-423
US-09-907-841-423
US-09-907-841-423
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US-09-906-742-423
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US-09-907-613-423
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US-09-907-842-423
US-09-904-859-423
US-09-904-859-423
US-09-904-859-423
US-09-904-859-423
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                                                                                                                                                                                                                                                                                                                                                                                                        1158786 seqs, 281726120 residues
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                                                                                                               - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT PILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US/01/41,048

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

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PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-11-39

PRIOR PILING DATE: 1999-11-39

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING D
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Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
                                                                                                                      Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth, J
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Gerritsen, Mary E.
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Gao, Wei-Qiang
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; ORGANISM: Homo
US-09-909-088B-423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATTHCQESEGHPRPHYSWYRNDVPL 180
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PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PELING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 2000-01-05
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Query Match Best Local Similarity 100.0 Matches 310; Conservative

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TYPE: PRT ORGANISM: Homo Sapien

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RESULT 2 US-09-909-088B-423

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NDRKEIDEIVIELTVOVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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100.0%; Score 310; DB 9; I
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0;
                                 PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1090-12-20
                      FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
PCT/US99/21090
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18-09-09-05-3-423
1 Sequence 423, Application US/09902853
2 Publication No. US20020192659A1
2 GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Baton, Dan L.
APPLICANT: Firrara, Napoleone
APPLICANT: Firvaroff, Blen
APPLICANT: Filvaroff, Blen
APPLICANT: Filvaroff, Blen
APPLICANT: Gao, Wei-Giang
APPLICANT: Gao, Wei-Giang
APPLICANT: Gerber, Hanspeter
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ORGANISM: Homo Sapien
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                                                                                                          SDPRIEWKKIODEQTTYVFFDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120
                                                                                                                                                                                           121 NDRKEIDKIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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                                             1 MALREPPRIALCARLPDFFILLLFRGCLIGAVNIKSSNRTPVVQBFESVELSCIITDSQT
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                    MALRRPPRIRICARLPDFFLLLLFRGCLIGAVNIKSSNRTPVVQEFESVELSCIITDSQT
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CURRENT PILING DATE: 2001-07-12

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PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-06

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

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PRIOR PILING DATE: 1999-09-08
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Eaton, Dan L.
Perrara, Napoleone
Pilvaroff, Bllen
Rong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Geritteen, Mary B.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Ashkenazi, Avi
Botstein, David
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                                                                                                          PIDSBANPRFRNSSFHLASETGTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMBVYDL
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,824

CURRENT FILING DATE: 2001-07-17

PRIOR PELICATION NUMBER: US/09/907,824

CURRENT FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/141,048

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-38

PRIOR PLING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PLING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: PCT/US99/21089

PRIOR APPLICATION NUMBER: PCT/US99/21089

PRIOR APPLICATION NUMBER: PCT/US99/21089

PRIOR APPLICATION NUMBER: PCT/US99/21089

PRIOR APPLICATION NUMBER: PCT/US99/21089
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Publication No. US20020197671A1
GENERAL INFORMATION:
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Pilvaroff, Bllen
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Gerritsen, Mary E.
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Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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Baton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR APLICATION NUMBER: US 60/143,048
PRIOR PLLING DATE: 1990-07-07
PRIOR APLLICATION NUMBER: US 60/145,698
PRIOR PLLING DATE: 1990-07-07
PRIOR PLLING DATE: 1990-07-28
PRIOR PLLING DATE: 1990-07-28
PRIOR PLLING DATE: 1990-07-28
PRIOR PLLING DATE: 1990-07-08
PRIOR PLLING DATE: 1990-09-08
PRIOR PLLING DATE: 1990-09-18
PRIOR PLLING DATE: 1990-09-15
PRIOR PLLING DATE: 1990-09-15
PRIOR PLLING DATE: 1990-09-15
PRIOR PLLING DATE: 1990-09-15
PRIOR PLLING DATE: 1990-10-15
PRIOR PLLING DATE: 1990-11-20
PRIOR PLLING DATE: 1990-12-06
PRIOR PRIOR PLLING DATE: 1990-12-06
PRIOR PLLING DATE: 1990-12-06
PRIOR PRIOR DATE: 1990-12-06
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CURRENT APPLICATION NUMBER: US/09/902,853
                                        Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                     Gurney, Austin L.
Hillan, Kenneth, J.
           Gerritsen, Mary E.
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Paoni, Nicholas F.
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Mather, Jennie P.
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Best Local Similarity 100.
Matches 310; Conservative
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; ORGANISM: Homo Sapien
US-09-902-853-423
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LENGTH: 310
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APPLICANT:
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61 SDPRIEWKKIODEQTTYVFPDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Acids Encoding the Same
FILLS REFERENCE: 10466-14
                                                                                                                                                                                                                                      PRIOR PAPLICATION NUMBER: US/09/907,841

CURRENT APPLICATION NUMBER: 2001-11-20

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 423

SECOND NOS: 423
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US-09-904-011-423
; Sequence 423, Application US/09904011
Mather, Jennie P.
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Best Local Similarity 100.1
Matches 310; Conservative
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US-09-907-841-423
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100.0%; Pred. No. 9.8e-293;
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              PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Goo, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
FILING DATE: 1999-11-29
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Best Local Similarity 100.
Matches 310; Conservative
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US-09-907-824-423
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APPLICANT: ROY, MAYGATER Ann APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel Millame, P. Mickey APPLICANT: Tumas, Daniel Millame, P. Mickey APPLICANT: Williame, I. Millame, I. TITLE OF INVENTION: Acide Encoding the Same TITLE OF INVENTION: Acide Encoding the Same FILE REFERENCE: 10466-14

FULE REFERENCE: 10466-14

CURRENT PILLING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US/65,350

PRIOR PILLING DATE: 2000-09-18

PRIOR PILLING DATE: 2000-09-18

PRIOR PILLING DATE: 2000-02-22

PRIOR PILLING DATE: 1999-07-07

PRIOR PILLING DATE: 1999-07-07

PRIOR PILLING DATE: 1999-07-07
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                                                                                                                                                                                                               1 MALIRIPPRINICARIPDFFILLIFRGCLIGAVNIKSSNRTPVVQBFBSVELSCIITDSQT 60
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                                                                                                         Gaps
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                                                   Length 310;
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                                                Query Match
100.0%; Score 310; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0;
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Grimaldi, Christopher
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Pilvaroff, Ellen
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Hillan, Kenneth, J.
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bottein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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US-09-904-011-423
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US-09-906-742-423
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CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
Publication No. US20030003530A1
GENERAL INFORMATION:
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Gerritsen, Mary B
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                        APPLICANT: Genentech, Inc.
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APPLICANT: Thumas, Daniel APPLICANT: Thumas, Daniel APPLICANT: Thumas, Daniel APPLICANT: Wood, Williams, P. Mickey APPLICANTON: Secreted and Transmembrane Polypeptides and Mucleic TITLE OF INVENTION: Acids Encoding the Same FILE PRETERENT 2001-07-16

REIGN PELLING DATE: 2001-07-16

REIGN PELLING DATE: 2001-07-16

REIGN PELLING DATE: 3000-02-27/US00/04414

REIGN PELLING DATE: 3000-02-27/US09/2034

REIGN PELLING DATE: 3000-02-13

REIGN PELLING DATE: 3009-02-13

REIGN PELLING DATE: 3009-02-13

REIGN PELLING DATE: 3009-03-13

REIGN PELLING DATE: 3009-03-13

REIGN PELLING DATE: 3009-10-15

REIGN PELLING DATE: 3009-11-20

REIGN PELLING DATE: 3009-11-20

REIGN REIGN PELLING DATE: 3009-11-20

REIGN REIGN REPLICATION NUMBER: PCT/US99/2031

REIGN REPLICATION NUMBER: PCT/US99/3031

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Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0;
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Grimaldi, Christopher J.
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Mather, Jennie P.
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Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Pilvaroff, Bllen
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Hillan, Kenneth, J
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Gao, Wei-Qiang
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US-09-906-838-423
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PRIOR FILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-28
PRIOR PELLICATION NUMBER: US 60/146,222
PRIOR PELLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20941
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
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Publication No. US20030027143A1
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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SEQ ID NO 423
LENGTH: 310
TYPE: PRT
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US-09-906-742-423
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US-09-906-838-423
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100.0%; Score 310; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-09-15
PRIOR PLLING DATE: 1999-10-05
PRIOR PLLING DATE: 1999-10-05
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-20
PRIOR PLLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLLING DATE: 1999-12-16
PRIOR PLLING DATE: 1999-12-16
PRIOR PLLING DATE: 1999-12-16
PRIOR PLLING DATE: 1999-12-20
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US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Betatein, David
; APPLICANT: Betatein, David
; APPLICANT: Beto, Dan L.
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Filvaroff, Ellen
Pong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423
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241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGBSYKNPGKPDGVNYIRTDEBG 300
                                                                                                                                                     61 SDPRIEWRKIQDEQTIYVPFDNKIQGDLAGRAEILGKTSLKIWNYTRRDSALYRCEVVAR 120
                                                                                                                                                                                                               NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                         121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSMYRNDVPL 180
                                                                                                                                                                                                                                                                                                        PIDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCBEQEMEVYDL 240
                            APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel B.
APPLICANT: Tumas, Daniel B.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                     PTDSRANPRFINSSFHLINSETGTLVFTAVHXDDSGQYYCIASNDAGSARCEEQEMEVYDL
                                                                                                                        SDPRIEWKKIQDEQTTYVPFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR
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PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USOU/04114
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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CURRENT FILING DATE: 2001-07-17
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Grimaldi, Christopher J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Publication No. US20030027145A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Perrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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us-09-524-531c-15.oli.rapb

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AFFLICANT: WOOG, WILLIAGH.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14

CURRENT PAPELICATION NUMBER: US/09/904,859

CURRENT PAPELICATION NUMBER: US/09/65,350

RIOR APPLICATION NUMBER: US/06/65,350

RIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-09

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
121 NDRKEIDEIVIKLTVQVKPVTFVCRVPKAVPVGKNATLHCQESEGHPRPHYSWYRNDVPL 180
121 NDRKEIDEIVIELTVQVKPVTFVCRVPKAVPVGKNATLHCQESEGHPRPHYSWYRNDVPL 180
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APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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Publication No. US20030036060A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary B.
Goddard, A.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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APPLICANT: Abkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/USO/04414
PRIOR PILING DATE: 1000-02-22
PRIOR PILING DATE: 1000-02-22
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PPLICATION NUMBER: PCT/US99/21090
PRIOR PPLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-05
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
                                                             Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                  Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
           Gerritsen, Mary E.
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Best Local Similarity 100.
Matches 310; Conservative
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TYPE: PRT
CRGANISM: Homo Sapien
US-09-907-942-423
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APPLICANT:
APPLICANT:
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APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Pani, James
APPLICANT: Stewart. Timoth A.
APPLICANT: Stewart. Timoth A.
APPLICANT: Timoth A.
APPLICANT: Timoth A.
APPLICANT: MOOd. William, I. y.
APPLICANT: Wood. Y. y.
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100.0%; Score 310; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.8e-293;
Matches 310; Conservative 0; Mismatches 0;
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US-09-909-204-423
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100.0%; Pred. No. 9.8e-293;
iive 0; Mismatches 0;
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-05
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
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PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
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US-09-204-423
Sequence 423, Application US/09909204
PUBLication No. US20030036061A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bettein, David
APPLICANT: Bettein, David
APPLICANT: Betton, Dan L.
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Filvaroff, Ellen
Pong, Sherman
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Gerritsen, Mary E.
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Best Local Similarity 100.0
Matches 310; Conservative
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ORGANISM: Homo Sapien
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; Pred. No. 9.8e-293;
0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: PCT/US99/30999
PRIOR PLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Williams, P. Mickey
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Tumas, Daniel
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Kljavin, Ivar J.
Mather, Jennie P.
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Gerritsen, Mary B.
Goddard, A.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 100.
Matches 310; Conservative
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Eaton, Dan L.
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Paoni, Nich
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US-09-904-820-423
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APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Paon, James
APPLICANT: Paon, Micholas F.
APPLICANT: Paon, Micholas F.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Milliam, P. Mickey
APPLICANTON NUMBER: US/09/904,820
CURRENT FILING DATE: 2001-07-13
FRIOR APPLICATION NUMBER: US 60/145,638
FRIOR PLING DATE: 1999-07-07
FRIOR PLING DATE: 1999-07-07
FRIOR PLING DATE: 1999-07-08
FRIOR PLING DATE: 1999-09-18
FRIOR PLING DATE: 1999-10-05
FRIOR PLING DATE: 1999-10-05
FRIOR PLING DATE: 1999-11-29
FRIOR PLING DATE: 1999-12-07
                         Sequence 423, Application US/09904820
Publication No. US20030036094A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
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Gerritsen, Mary B.
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Botstein, David
Desnoyers, Luc
Baton, Dan L.
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241 NIGGIIGCVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OP INVENTION: Acids Encoding the Same PILE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,786

CURRENT APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

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SEQ ID NO 423

LENGTH: 310
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CORGANISM: Homo Sapien
US-09-904-786-423
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OM protein - protein search, using sw model

Run on:

June 15, 2004, 11:06:35; Search time 14 Seconds (without alignments) 2129.955 Million cell updates/sec

US-09-524-531C-15

310 1 MALRRPPRLRLCARLPDFFL.......VNYIRTDBBGDFRHKSSFVI 310 Perfect score:

Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283366 seqs, 96191526 residues 0 Word size : Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	MHC class I lympho	probable RING zinc	MHC class I histoc	type I restriction	class I histocompa	class I histocompa	class I histocompa	HLA-C alpha chain	probable membrane	carbon starvation	lymphotoxin beta -	hypothetical prote		hypothetical prote	hypothetical prote		ical	partial probable s	partial probable s	GTP-binding protei	GTP-binding protei	hypothetical prote	phosphatidylserine	occlusion-derived	cobalt transport p	lymphotoxin beta -	transcription regu	epidermal autoanti	phosphate ABC tran
SUMMARIES	QI	168750	AB6406	HLHUC4	E82933	JH0546	JH0547	JH0545	137078	AB1013	A86676	-	AH1748	G70548	T08548	T01282	B90241	T25730	B85833	B90988	T03627	T01588	E86888	T47268	T30446	G84315	A46066	T35883	PH0269	H84023
	Length DB	290 2	336 2	342 1	•	366 2	366 2	366 2	366 2	492 2	784 2	•	113 2	171 2	172 2	173 2	173 2	173 2	177 2	177 2	208 2	208 2	•	214 2	217 2	242 2	244 2	255 2	280 2	294 2
عد	Query Match I	2.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3
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	Result No.	-	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

hypothetical prote conserved hypothet nitrate transport probable lipoprote heat shock protein lymphotoxin-beta - hypothetical prote sugar transport sy hypothetical prote G protein-coupled probable sugar ABC conserved hypothet	GGDEF family prote hypothetical prote hypothetical prote protein R74.2 [imp
AB3037 AB1002 A98249 A98249 A62017 I49139 I49133 T27302 T27302 H95879	G75614 T46378 F71815 B88421
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297 2997 300 300 314 314 348	362 375 376 380
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4 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 ርን EC 4 2

## ALIGNMENTS

MHC class I lymphocyte antigen - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 21-Jan-2000
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 21-Jan-2000
C;Accession: 16950
R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, B.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B
A;Reference number: 154457; MUID:89233295; PMID:2714852

A, Accession: 168750
A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: mRNA

A;Residues: 1-290 <RES> A;Cross-references: GB:M28207; NID:g576478; PIDN:AAA53259.1; PID:g576479 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology F;144-209/Domain: immunoglobulin homology <IMM>

Length 290; 0; Indels 2.6%; Score 8; DB 2; 100.0%; Pred. No. 5.8; ative 0; Mismatches Query Match
Best Local Similarity 100.
Matches 8; Conservative

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Gaps

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249 VLVVLAVL 256 ò

241 VLVVILAVI, 248

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RESULT 2

probable RING zinc finger protein [imported] - Arabidopsis thaliana probable RING zinc finger protein [imported] - Arabidopsis thaliana (mouse-ear cress) C.jSpecies: Arabidopsis thaliana (mouse-ear cress) C.jSpecies: Arabidopsis thaliana (mouse-ear cress) C.jSpecies: Arabidopsis thaliana (mouse-ear cress) C.jAccession: A86406 C.jAccession: Arabidopsis thaliana (Arabidopsis C.jAccession: A86406 C.jAccession: Arabidopsis thaliana (Arabidopsis C.jAccession: A86406 C.jAccession: Arabidopsis C.jAccession: A86406 C.jAccession: Arabidopsis C.jAccession: A86406 C.jAccession: Arabidopsis C.jAccession: A86406 C.jAccession: Arabidopsis C.jAccession: A86406 C.jAccession: Aaccession: Aaccession: Aaccession: Aaccession: Aaccession: Aaccession: Aaccession: Aaccession: A

A;Status: preliminary

A;Cross-references: GB:AE005172; NID:g11024872; PIDN:AAG26956.1; GSPDB:GN00141 A;Molecule type: DNA A;Residues: 1-336 <STO>

A; Map position: 1

gorilla

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C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: transmembrane protein
C; Keywords: transmembrane protein
P; 1-24/Domain: signal sequence #status predicted <SIG>
E; 25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0203 #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introne: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Kaywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
P;25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0202 #status pr
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C; Species: Gorilla gorilla gorilla (lowland gorilla)
C; Date: 30-Unn-1992 #sequence_revision 30-Unn-1992 #text_change 23-Unl-1999
C; Accession: JH0547
R; Lawlor, D.A.; Warren, B.; Taylor, P.; Parham, P.
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to human A; Reference number: JH0534; MUID: 92078860; PMID:1744581
                                                                                           class I histocompatibility antigen Gogo-CO202 heavy chain precursor - lowland C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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A;Residues: 1-366 <LAM>
A;Cross-references: BNBL:X60248; NID:g22884; PIDN:CAA42800.1; PID:g22885
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X60249; NID:g22882; PIDN:CAA42801.1; PID:g22883
A;Experimental source: EBV-transformed B cell
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F;25-114/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;207-285/Domain: alpha-3 <AL3>
F;220-285/Domain: intracellular #status predicted <INT>
F;299-366/Domain: intracellular #status predicted <INT>
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F;207-298/Domain: alpha-3 <AL3>
F;207-285/Domain: immunoglobulin homology <IMM>
F;207-285/Domain: immunoglobulin homology <IMM>
F;299-366/Domain: intracellular #status predicted <INT>
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100.0%; Pred. No. 7.1
tive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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A; Residues: 1-366 < LAW>
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                        RESULT 3
HIATUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C; Species: Homo sapiens (man)
C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C; Accession. A24512
R; Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A; Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A; Reference number: A92500; MUID:86033791; PMID:3863816
A; Accession: A24512
A; Molecule type: DNA
A; Residues: 1-342 - DAV>
A; Cross-references: GB:M11886; NID:g184173; PIDN:AA52665.1; PID:g386777
C; Genetics:
A; Gene: GDB:HLA-C
A; Cross-references: GB:M1931; OMIM:142840
A; Map position: 6621.3-5621.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F; 196-261/Domain: immunoglobulin homology < IMM>
F; 86/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma ure C; Species: Ureaplasma urealyticum S; Stacession: B82303 R; Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. Bubmitted to GenBank, February 2000 A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir A; Reference number: A82810 A; Retension: Prelimiary A; Molecule type: DNA A; Status: prelimiary A; Molecule type: DNA A; Resference number: B82333 A; Status: prelimiary A; Molecule type: DNA A; Cross-references: GB:AE002110; GB:AF222894; NID:G6899051; PIDN:AAF30504.1; GSPDB:GN001 A; Experimental source: Berovar 3; biovar 1 C; Genetics: A; Genetics: A; Genetics: A; Genetic code: SGC3 C; Superfamily: type I site-specific deoxyribonuclease chain hsdM
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             Length 336;
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100.0%; Pred. No. 6.7;
tive 0; Mismatches
      2.6%; Score 8; DB 2;
100.0%; Pred. No. 6.6;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
                                          Best Local Similarity 100.
Matches 8; Conservative
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             Query Match
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JH0546
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Gapa

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0; Indels

Length 366,

DB 2;

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RESULT 7
JH0545
class I histocompatibility antigen Gogo-C0201 heavy chain precursor - lowland gorilla
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                             Gaps
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Length 366;
                             Indels
DB 2;
2.6%; Score 8; DB 2
100.0%; Pred. No. 7.1
:ive 0; Mismatches
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Gaps

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Ribolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis & A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86676
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbon starvation protein [imported] - Lactococcus lactis subsp. lactis (strain ILL403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: A86676
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C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 05-Nov-1999
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 05-Nov-1999
C;Accession: UCS645
R;Watzocha, K.; Renard, N.; Charlot, C.; Bienvenu, J.; Coiffier, B.; Salles, G.
Biochem. Biophys. Res. Commun. 238, 273-276, 1997
A;Title: Identification of two lymphotoxin beta isoforms expressed in human lymphoid ce
A;Reference number: UCS645; MUID:97445965; PMID:9299492
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sert A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-784 <STO>
A;Cross-references: GB:AE005176; PID:g12723283; PIDN:AAK04507.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                           A;Residues: 1.492 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09203.1; PID:g16505207; GSPDB:GN00176
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2.3%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 14;
Conservative 0; Mismatches
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100.0%; Pred. No. 9.2;
vative 0; Mismatches
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N;Alternate names: non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: carbon starvation protein
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 IGGIIGGV 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 VLAVLALI 230
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hes 8, Conserv
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A; Residues: 1-77 <WAR>
                                                                                                       A;Accession: AB1013
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                   A; Gene: STY4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                     C; Genetics:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Aintrons: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre P; 25-366/Product: class I histocompatibility antigen heavy chain, Gogo-C0201 #status pre P; 25-114/Domain: alpha-1 < ALI>
P; 115-206/Domain: alpha-2 < ALI>
P; 200-288/Domain: alpha-3 < ALI>
P; 200-285/Domain: immunoglobulin homology < IMM>
P; 299-366/Domain: intracellular #status predicted < INT>
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S.Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: AB1013
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.Parkhill, J.; Dougan, G.; James, R.D.; Thomson, N.R.; Pickard, Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
   C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0545
R;Lawlor, D.A.; Warren, B.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A;Reference number: JH0545
A;Moleque type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA-C alpha chain - human (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: 137078
E;Vilches, C.; Bunce, M.; de pablo, R.; Herrero, M.J.; Kreisler, M.
Tissue Antigens 46, 19-23, 1995
A;File: Anchored PCR cloning of the novel HIA-Cw*0704 allele detected by PCR-SSP.
A;Reference number: I37078; WUID:96086482; PMD:17482492
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                            A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60251; NID:g22880; PIDN:CAA42803.1; PID:g22881
A;Experimental source: EBV-transformed B cell
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A;Molecule type: mRNA
A;Residues: 1-366 <RES>
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100.0%; Pred. No. 7.1;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 7.1
Matches 8; Conservative 0; Mismatches
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Matches 8; Conservative
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R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; M. submitted to the Protein Sequence Database, May 1999
A;Reference number: 216442
A;Reference number: 216442
A;Reference TY08548
A;Molecule type: DNA
A;Residues: 1-17 cBEV.
A;Reperimental source: cultivar Columbia; BAC clone F27813
                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 7; DB 2;
100.0%; Pred. No. 39;
tive 0; Mismatches
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Job time : 15 secs
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Best Local Similarity 100.
Matches 7; Conservative
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A;Gene: At2g19340; F27F23.14
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37 RPPRLRL 43
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A,Gene: ATSP:F27B13.110
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                                                                                                                                                            AMINGOLDERICAL protein lin2533 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
S;Gecession: AH1748
D; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, U.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Nethors: Kreft, U.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Neteeroce number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AH1748
A;Status: preliminary
A;Kesidues: 1-113 <cLAb
A;Coss-references: GB:AL592022; PIDN:CAC97760.1; PID:g16415055; GSPDB:GN00178
A;Residues: 1-113 dGLAb
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Dates: 17-011-1998 #sequence_revision 17-011-1998 #text_change 28-Ju1-2000
C;Accession: G70548
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70548
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-171 <COL>
A;Cols Sereferences: GB:29558; GB:AL123456; NID:g3261781; PIDN:CAB08967.1; PID:e316801; A;Experimental source: strain H37Rv
C;Genetics:
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100.0%; Pred. No. 27;
tive 0; Mismatches
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                    40 VLAVLAL 46
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Best Local Similarity
Matches 7; Conserv
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hypothetical protein At2g19340 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein P27F23.14
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T01282; B84575
C;Accession: T01282; B84575
Submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC P27F23 genomic sequence.
A;Reference number: 214177
                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T01222
A; Status: translated from GB/BMBL/DDBJ
A; Status: translated from GB/BMBL/DDBJ
A; Status: translated from GB/BMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-173 <ROUJ>
A; Cross-references: EMBL:AC003058; NID:g3135250; PID:g3135264
A; Experimental source: cultivar Columbia
R; Lin, X.; Raul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; K.Co., H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
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A Modecule type: DNA
A Residues: 1-773 cSTC>
A;Cross-references: GB:AE002093; NID:g3135264; PIDN:AAC16464.1; GSPDB:GN00139
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C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 22-Oct-1999

C;Accession: T08548

hypothetical protein F27B13.110 - Arabidopsis thaliana

RESULT 14

· 7

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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1997 (Rel. 25, Last annotation update)
01-NOV-1997 (Rel. 25, Last annotation update)
Class I histocompatibility antigen, GOGO-C0201 alpha chain precursor.
Gorilla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
688
693
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729
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                                                                                                                                                                                                                                                         STANDARD:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AA;
 TX3A PHONI
ID TX3A PHONI
AC P81793;
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P30385;
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SIGNAL
PROPEP
CHAIN
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gorilla gor
gorilla gor
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mus musculu
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1614.175 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             310
1 MALRRPPRIRICARLPDFFL.......vnyirtdeegdfrhkssfvi 310
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P30387
P10321
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940800
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P11168
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O29490
                                                                                           June 15, 2004, 11:05:10; Search time 10 Seconds
               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  Notal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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HINC PARTE
HIPX AGUME
TINEC MOUSE
TINEC MARNO
GRRB HUMAN
HAD METVO
TINEL SCOLI
PVR HUMAN
SYTE MOUSE
APY SOLTU
LARRA STELN
CPBA RABIT
CPBA RABIT
CPBA RABIT
GTRZ HUMAN
IRLA MOUSE
IRLA MOUS
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S212 HUMAN
S212 MOUSE
S212 RAT
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1C03_GORGO
1C04_GORGO
1C07_HUMAN
1C18_HUMAN
1C18_HUMAN
YGIK_SALTY
TATB_STRCO
XLR1_MOUSE
RS2_SHEON
                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TX3A_PHON
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Match
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Maximum DB seq
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                                                                  OM protein
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                                                                                                                                                                             Sequence:
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                                                                                            Run on:
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No.
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TISSUENCE FROM N.A.

TISSUE-Venom gland;

MEDLINE-99053416; PubMed=9839681;

Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.P.,

Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.P.,

Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.P.,

Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.P.,

Cordairo M.N., Beirao P.S.L.;

Gomez M.V., Beirao P.S.L.;

"Cloning, CDNA sequence analysis and patch clamp studies of a toxin

"Cloning, CDNA sequence analysis and patch clamp studies of a toxin

"Consignal CDNA sequence analysis and patch clamp studies of a toxin

"Toxicon 36:1971-1980(1998).

"Toxicon 36:1971-1980(1998).

"I FUNCTION: Anagonist of L-type calcium channels (By similarity).

"I SUBJEBLUIAR LOCATION: Secreted.

"I SIMILARITY: Belongs to the spider toxin Tx3 family.

InterPro; IPRO04169; spidertoxin.

"Toxicon PRO2819; spidertoxin; IncerPro; Inhibitor; Calcium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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arabidopsis
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escherichia
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saccharomyc
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                                                  aspergillus
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rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phoneutria nigriventer (Brzzilian armed spider).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae;
Araneomorphae, Entelegynae, Lycosoidea, Ctenidae, Phoneutria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
006584 | 000141 | 000141 | 000141 | 00184 | 00184 | 0018759 | 0018759 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001877 | 001
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BY SIMILARITY.
NEUROTOKIN PN3A.
BY SIMILARITY.
BSBP209257EB6793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin Pn3A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                               YJIY_ECOLI
GOAS_MOUSE
SCIB_YEAST
CCIG_YEAST
RPS2_ARATH
SCA4_RICFE
K6PI_CANAL
SCA4_RICSI
SCA4_RICSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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100.0%; Pre
         PYS2
NCPR
TGM2
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37
71
80
8937 MW;
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366 AA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             Lawlor D.A., Warren B., Taylor P., Parham P., "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.", "d. Exp. Med. 174:1491-1509[1991].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
class I histocompatibility antigen, GOGO-CO203 alpha chain precursor.
Gorilla gorilla Gorilla (Lowland gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92078860; PubMed=1744581;
Lawlor D.A., Warren B., Taylor P., Parham P.;
"Gorilla class I major histocompatibility complex alleles: comparison
                                                                                                           immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
40782 MW; 11CCAD1F6091831B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal.

4 CLASA I HILARITY.

6 CLASA I HISTOCOMPATIBILITY ANTIGEN,

GOGO-CO202 ALPHA CHAIN.

4 EXTRACRILULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 8; DB 1;
100.0%; Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
BY SIMILARITY
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InterPro; 1PR007110; Ig-like.
InterPro; 1PR007110; Ig-like.
InterPro; 1PR003597; Ig_c1.
InterPro; 1PR001039; MHC.
InterPro; 1PR001039; MHC.
InterPro; 1PR001039; MHC.
I.
Pfam; PP00047; Ig; 1.
PR.NTS; PR01639; MHCCLASSI.
ProDom; PD000050; MHC.
I; 1.
PROSITE; PS00299; IG_LIKE; 1.
PROSITE; PS00299; IG_LIKE; PALSE_NEG.
MEDLINE=92078860; PubMed=1744581;
                                                                                                                                                                                                                                                                                                                                   EMBL; X60249; CAA42801.1; -. PIR; JH0546; JH0546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 VLVVLAVL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 VLVVLAVL 324
                                                                                                                                               microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 AA;
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1115
207
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333
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227
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DOMAIN
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SEQUENCE
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1C04_GORGO
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                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BYBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.sib.ch).
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                                                                      Lawlor D.A., Warren B., Taylor P., Parham P.,
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.",
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last samotation update)
Class I histocompatibility antigen, GOGO-C0202 alpha chain precursor.
Gorilla gorilla (Lowland gorilla).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararthini; Hominidae; Gorilla.
                                                                                                                                                                  immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain {beta-2-
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BY SIMILARITY.

CLASS I HISTOCOMPATIBILITY ANTIGEN, GGOC-C201 ALPHA CHAIN.

EXTRACELLULAR ALPHA-1.
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (B)
058159364C769FC5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P30665; 1A9E.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig c1.

DR InterPro; IPR003597; Ig c1.

DR InterPro; IPR003006; Ig WHC.

DR Pfam; PP00497; Ig; I.

DR Pfam; PP00129; WHC_I.

DR Pfam; PR0129; WHC_I.

DR PRINTS; PR01638; WHCLIASI.

R SWART; SM0407; IGc1; I.

R PROSITE; PS00290; IG HHC; PALSE NEG.

MHC I; Transmembrane; Glycoprotein. c1.

SIGNAL.
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100.0%; Pred
0; M
                                   SEQUENCE FROM N.A.
MEDLINE=92078860; PubMed=1744581;
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Best Local Similarity 100.
8. Conservative
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                                                                                                                                                                                                           microglobulin).
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 NCBI_TaxID=9595;
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DOMAIN TRANSMEM

DOMAIN

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CARBOHYD SEQUENCE DISULPID

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Gaps

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GORGO

1C03\_GORGO RESULT 3

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P30386;

us-09-524-531c-15.oli.rsp

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Tissue Antigens 44:268-270(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coulie P.G.;
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
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                                                                          -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
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P10321; 078061; 078083; 029631; 029652; 029867; 029990; 095463; 095603; 09M731; 09TQP9; 01-MAR-1989 (Rel. 10, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
HLA class I histocompatibility antigen, Cw-7 alpha chain precursor (MHC class I antigen Cw*7).
Homo class I antigen Cw*7).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-CO203 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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MEDLINE=9116330; PubMed=7871529;
Steinle A., Schendel D.J.;
ALHA Class I allelse of LCL 721 and 174xCEM.T2(T2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNECTING PEPTIDE
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Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00129; MILLY, PRINTERS; PR01639; MHCCIASSI.
SMART; SM00407; IGC1; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00839; IG LIKB; 1.
PROSITE; PS00209; IG MHC; FALSE NEG.
MHC I; Transmembrane; Glycoprotein; Signal.
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BY SIMILARITY.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PP00047; ig; 1.
Pfam; PP00129; MHC_I: 1.
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308
332
366
1188
283
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366 AA;
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                                                             immune system.
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TRANSMEM
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SEQUENCE OF 26-338 FROM N.A. (CW*0701).
MEDLINE=99416847; Pubmed=10489744;
Van der Vlies S.A., Voorter C.B., van den Berg-Loonen E.M.;
"There is more to HLA -C than exons 2 and 3: sequencing exons 1, 4 and
                        WEDLINE-89233295; PubMed-2714852;
Pohla H., Kuon W., Tabaczewski P., Doerner C., Weiss B.H.;
"Allalic variation in HLA-B and HLA-C sequences and the evolution of
the HLA-B alleles ";
Immunogenetics 29:297-307(1989).
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MEDLINE=86033791; PubMed=3863816;
Davidson W.F., Kress M., Khoury G., Jay G.;
Comparison of HLA class I gene sequences. Derivation of
HLA-C genes.";
Jocus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
HLA-C genes.";
J. Biol. Chem. 260:13414-13423(1985).
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MEDLINE=97161041; PubMed=9008313;
Vilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreigler M.;
FMOJecular cloming of two new HiA-C alleles: Cw*1801 and Cw*0706.";
Tissue Antigens 48:698-702(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang H., Tokunaga K., Ishikawa Y., Asahina A., Kuwata S., Akaza T., Tadokoro K., Shibata Y., Takiguchi M., Juji T.; "Identification and DNA typing of two Cw7 alleles (Cw*0702 and Cw*0704) in Japanese, with the corrected sequence of Cw*0702.";
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MEDLINE=98349393; PubMed=9686604;
Turner S., Bllexson M.B., Hickman H.D., Sidebottom D.A.,
Pernandez-Vina M., Confer D.L., Hildebrand W.H.;
"Sequence-based typing provides a new look at HLA-C diversity.";
J. Immunol. 161:1406-1413(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cooper S.L., Adams E.J., Wells R.S., Walker C.M., Parham P.; "A major histocompatibility complex class I allele shared by two species of chimpanzee.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-22512041; PubMed=12622774;
Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
Madrigal J.A., Little A.-M.;
"Cloning and sequencing full-length HLA-B and -C genes.";
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MEDLINE=96086482; PubMed=7482492;
Wilches C., Bunce M., de Pablo R., Herrero M.J., Kreisler M.;
"Anchored PCR cloning of the novel HLA-Cw*0704 allele detected PCR-SSP.";
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (CW*0702 AND CW*0704).
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SEQUENCE OF 77-309 PROM N.A. (CW*0701).
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MEDLINE=98099755; PubMed=9435339;
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N -> K (in allele Cw*0702, allele
Cw*1703, allele Cw*0704 and allele
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MEDIATRS=97161041; PubMed=900813;
Wilches C., Bunce M., Sanz L., de Pablo R., Puente S., Kreisler M.;
"Molecular cloning of two new HLA-C alleles: Cw*1801 and Cw*0706.";
                                                                                 /FTId=VAR 016590.
S -> N (in allele Cw*0709).
/FTId=VAR 016591.
N -> K (in allele Cw*0709).
FTId=VAR 016592.
L -> P (in allele Cw*0704 and allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_016647.
/FTId=VAR_016647.
Cw0711}.
                                                                                                                                                                                                                                                                                                                                                                                                                              D (in allele Cw*0704 and allele
                                                                                                                                                                                                                                        /PTId=VAR_016593.
{ -> S (in allele Cw*0702 and allele
                                                                                                                                                                                                                                                                                                     PTIG=VAR_016594.
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MEDLINE=22512041; PubMed=12622774;
Cox S.T., McWhinnie A.J., Robinson J., Marsh S.G.E., Parham P.,
Madrigal J.A., Little A.-M.;
"Cloning and sequencing full-length HLA-B and -C genes.";
Tissue Antigens 61:20-48(2003).
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100.0%; Pred. No. 5.5;
ive 0; Mismatches 0; Indel8
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/FTId=VAR 016598.
A -> V (in allele Cw*0706).
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T -> A (in allele Cw*0711)
                                                                                                                                                                                                                                                                                                                                                                                    CW*0703)
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8
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L -> W (in allele
/FTId=VAR 016646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTIG=VAR 016600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_016596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTIG=VAR_016597
                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> D (i
Cw*0711).
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nes 8; Conservative
          110
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             CARBOHYD
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                                MEDLINE-99299762; PubMed=10372547;
MEDLINE-99299762; PubMed=10372547;
MEDLINE-99299762; PubMed=10372547;
MEDLINE-99299762; PubMed=10372547;

"Correction of HiA-Cw+0501 and identification of HiA-Cw+0711.";

Tissue Antigens 53:510-512(1999).

-!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.

-!- SUBMNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).

-!- SUBMNIT: Heterodimer of membrane protein.

-!- POLYMORPHISM: The following alleles of Cw-7 are known: Cw+0701, Cw+0703, Cw+0706, Cw+0706, Cw+0709 and Cw+0711. The sequence shown is that of Cw+0701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC 1; 1.
PFADTS: PR01639; MHC 1; 1.
SMART; SM00407; IGc1; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS0835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; PALSE NEG.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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BY SIMILARITY.
BY SIMILARITY.
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AJ293016; CAC04321.1; -.
AJ293017; CAC04322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF015557; AAC17722.1; -. AF015556; AAC17722.1; JOINED. AJ010749; CAA09341.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y18533; CAB71800.1;
Y18534; CAB71800.1; JOINED.
Y18535; CAB71800.1; JOINED.
Y18536; CAB71800.1; JOINED.
PD3826; BAA07531.1;
PD49819; BAA08625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ291815; CAC19191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z46810; CAA86840.1; -. M28207; AAA53259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X83394; CAA58313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U09853; AAA50217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M11886; AAA52665.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:4933; HLA-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X97321; CAA65986.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X83394; CAAS8313
BMBL; U09853; AAA50217
EMBL; X97311; CAA5596
EMBL; AA7015557; AAC1777
EMBL; AA7010749; AAC1777
EMBL; AA1010749; AAC1777
PIR; AA512; HLHUC4.
PIR; 137078; 137078.
PIR; 137529; 137529.
PIR; 168750; 168750.
HSSP; P10466; 1AGD.
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1115
207
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309
334
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227
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DOMAIN
TRANSMEM
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EMBL;
EMBL;
EMBL;
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EMBL;
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Gaps

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317 VLVVLAVL 324
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                                                                                         YGIK SA
P40800;
               셤
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                                                         Tiercy J.M.;
"Sequence of four new HLA-Cw alleles: a possible role of interallelic
recombination.";
                                                                                                                                                                                                                                        -!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                        "The novel HLA-Cw*1802 allele is found associated with B*5703 in the Bubi population from Equatorial Guinea.";
Tissue Antigens 49:644-649(1997).
                                                                                                                                                                                                                                                     immune system.
SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (BY SIMILARITY).

V -> A (in allele Cw*1802).

FTIG=VAR 016615.

67CF7E94884327D8 CRC64;
                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein.
POLYMORPHISM: The following alleles of Cw-18 are known: Cw*1801 (Cw*04GB) and Cw*1802 (Cw*18GB). The sequence shown is that of
                                                                                                                                SEQUENCE FROM N.A. (CW*1802).
MEDLINE-97378891; PubMed=9234488;
Vilches C., Bunce M., de Pablo R., Moreno M.B., Puente S., Sanz L.,
Kreisler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASS I HISTOCOMPATIBILITY ANTIGEN
                                             Grundschober C., Labonne M., Javaux P., Steiner Q.G., Gebuhrer L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6%; Score 8; DB 1; Length 366;
100.0%; Pred. No. 5.5;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW-18 ALPHA CHAIN
               (CW*1801).
              SEQUENCE OF 26-206 FROM N.A. (CW*
MEDLINE=98119594; PubMed=9459506;
                                                                                                     Tissue Antigens 51:72-79(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PP00047; ig; I.
Pfam; PP00129; MHC_I.
PRINTS; PR01638; NHCCLASSI.
ProDom; PD000050; MHC I; I.
SMART; SM0407; IGC1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X96582; CAA65401.1; -.
EMBL; AJ420253; CAD12438.1; -.
EMBL; Z80227; CAB02408.1; -.
EMBL; Y09156; CAA70354.1; -.
HSSP; P30460; IAGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3enew; HGNC:4933; HLA-C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 142840;
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DOMAIN
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B., Ryan E., Sun H., Plorea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                     Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                               Cong J., Schmid M.B.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A -> R (IN REF. 1).
A -> P (IN REF. 1).
BEA79EFCFEEBA58A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  (Probable).
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. 6.4;
                                     (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 8; DB 1
llarity 100.0%; Pred. No. 6.4
Conservative 0; Mismatches
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POTENTIAL.
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PRT;
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EMBL; AE008845; AAL22045.1; -.
                          (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46004 MW;
                                                 28-FEB-2003 (Rel. 41, Last
Hypothetical protein ygiK.
YGIK OR STM3171.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 8; Conserv
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                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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146
176
226
280
                                                                                                                                NCBI_TaxID=602;
                       01-FEB-1995
28-FEB-2003
                                                                                                                                                                       STRAIN=LT2;
SALTY
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Gaps

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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Eye;
Brunner B., Todt T., Lenzner S., Stout K., Schulz U., Ropers H.-H.,
                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                               "Genomic structure and comparative analysis of seven contiguous gendisclose a large region with conserved gene order in human Xp22.2-
           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Retinoschisin precursor (X-linked juvenile retinoschisis protein
                                                                                                                                                                                                                       MEDLINE=99160474; PubMed=10051329;
Gehrig A.E., Warneke-Wittstock R., Sauer C.G., Weber B.H.F.;
"Isolation and characterization of the murine X-linked juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99148018; PubMed=10023077;
Reid S.N., Akhmedov N.B., Piriev N.I., Kozak C.A., Danciger M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The mouse X-linked juvenile retinoschisis cDNA: expression in
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     retinoschisis (Rs1h) gene.";
Mamm. Genome 10:303-307(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 227:257-266(1999).
                                                                                           AS1 OR RS1H OR XLRS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROM N.A.
                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Kalscheuer V.M.;
                                                                                                                                                                                                           STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parber D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Required for correct localization of precursor proteins bearing signal peptides with the twin arginine conserved motif S/T-R-R-X-F-L-K. This sec-independent pathway is termed TAT for twin-arginine translocation system. This system mainly transports proteins with bound cofactors that require folding prior to export (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A., "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00237; -; 1.
InterPro; IPR003998; TatB.
PRINTS; PR01506; TATBROTEIN.
Transport; Protein transport; Translocation; Transmembrane; Membrane; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%; Score 7; DB 1; Length 161;
100.0%; Pred. No. 27;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                         Sec-independent protein translocase protein tatB homolog. TATB OR SCO5150 OR SCP8.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
, 0510C0D221BEBER3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LÓCATION: Membrane-bound (Probable).
                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                              161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL939122; CAC01351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 161 AA; 17757 MW;
                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 417:141-147(2002)
                                                                                                                              STANDARD;
                                                                                                                                                                                                                                              Streptomyces coelicolor
                  242 IGGIIGGV 249
                                                236 iéciiécy 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 LVVLAVL 256
                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=1902;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                  Astraubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Riausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Riachul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rachas S., McZewan P.J., McKernan K.J., Malek J.A., Gunzaren P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myere R.M.,
Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Reneratical A., Schain J.B., Jones S.J.M., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: May be active in cell adhesion processes during retinal development (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: Retinal specific.
MEDLINE=22388257; PubMed=12477932;
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224 AA.

PRT;

STANDARD;

XLR1 MOUSE ID XLR1 MOUSE

RESULT 9

13 LWLAVL 19

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PDGVNYI 294
                                                                                                                                                                                      193 PDGVNYI 199
                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 TISSUE-T-cell;
                                                                                                                                                                    288
                                                                                                                                                                                                                            TNFC_HUMAN
                                                                                                                                                  Matches
                                                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Debor T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mullerler J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
-!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                     2.3%; Score 7; DB 1; Length 224; 100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                   4536203CC00E90E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
10S ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                          242 AA
                                                                                                                                                                                                       RETINOSCHISIN.
                                                                                                                                                                                                                 F5/8 TYPE C.
BY SIMILARITY.
                                                                                                                                                                                                                                                            100.0%; Prec. ...
0; Mismatches
                        email to license@isb-sib.ch)
                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                   X
                                                                                                                                                                                                                                   25575
                                                                                                                                                                                                                                                              Local Similarity 100.
108 7; Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                      18 PPLLLLP 24
                                                                                                                                                                                                                                   224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
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send an
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OBECHS:
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                                                                                                                                                                                                                                   SEQUENCE
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Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWPC HUMAN STANDARD; PRT; 244 AA.

Q0664); P78370; Q99761;
Q10664); P78370; Q99761;
Q10664); P78370; Q99761;
Q10664); P78370; Q99761;
Q1070N-1994 (Rel. 29, Last sequence update)
UJWAR-2004 (Rel. 43, Last sequence update)
Lymphotoxin-beta (LT-beta) (Tumor necrosis factor (TNF-C) (Tumor necrosis factor ligand superfamily member 3).
HOWO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salles G.; "Identification of two lymphotoxin beta isoforms expressed in human lymphoid cell lines and non-Hodgkin's lymphomas."; Biochem. Biophys. Res. Commun. 238:273-276 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE PROM N.A. (ISOPORM 1).

SOWEN L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

Lasky S., Hood L.;

"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Browning J.L., Ngam-Bk A., Lawton P., Demarinis J., Tizard R., Chow B.P., Hession C. O'Brine-Greco B., Foley S.F., Ware C.F.; Fupphotoxin beta a novel member of the TNF family that forms a heteromeric complex with lymphotoxin on the cell surface."; Cell 72:847-856 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
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"A new member of the immunoglobulin superfamily and a V-ATPase G
subunit are amongst the predicted products of novel genes close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=97445965; PubMed=9299492;
Warzocha K., Renard N., Charlot C., Bienvenu J., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indele
                                                         HAWAF; MF 00291; -; 1.
InterPro; IRR001865; Ribosomal S2.
InterPro; IRR005706; Ribosomal S2.
FRINTS; PRO0395; RIBOSOWALS2.
FRINTS; PRO0395; RIBOSOWALS2.
TIGRPAMS; TIGR01011; rpsB bact; 1.
PROSITE; PS00962; RIBOSOWAL_S2.1; 1.
PROSITE; PS00963; RIBOSOWAL_S2.2; 1.
Ribosomal protein; Complete proteone.
SRQUENCR 242 AA; 26569 WW; 74AA24550750B88C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF locus in the human MHC.";
Submitted (SEP-1997) to the RMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. Mc.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; Fred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93208881; PubMed=7916655;
EMBL; AB015609; AAN54684.1; -.
TIGR; S01629; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
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                                                                                                                                      SEQUENCE FROM N.A. (ISOPORM 1), AND VARIANTS ARG-84 AND PHE-87.

Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (JAN-2003) to the EMBL/GenBank/DOBJ databases.

--- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific role in immune response regulation. Provides the membrane anchor for the attachment of the heterotrimeric complex to the cell surface. Isoform 2 is probably non-functional.

--- SUBUNIT: Heterotrimer of either two LTB and one LTA submits or (less prevalent) one LTB and two LTA submits.

--- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing; Polymorphism.

DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).

TOTAL SMITTER 19 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                      Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth B.J., Yi Q., Nickerson D.A.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-70 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1soId=006643-2; Sequence=VSP 006441, VSP_006442;
-!- TISSUB SPECIFICITY: Spleen and thymus.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0015070; F:roxin activity; NAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006053; TNP family.
InterPro; IPR008093; TNP family.
InterPro; IPR008093; TNP subf.
Pfam; PF00229; TNP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q06643-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, L11016; AAA99888.1; -.
EMBL, 108922; AAC51769.1; -.
EMBL, U79029; AAB37342.1; -.
EMBL, L11015; AAB37342.1; -.
EMBL, T47768; CAA75069.1; -.
EMBL, RP129756; AAB161089.1; -.
EMBL, RP129756; AAB161089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY070219; AAL49954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY070219; AAL49955.1; -. AY216497; AA021134.1; -.
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PIR; JC5445; JC5645.
HSSP; P01374; ITNR.
Genew; HGNC:6711; LTB.
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EMBL;
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CARBOHYD

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KQISAPGSQLPTS (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.

MEDLINE=22709134; PubMed=12799463;

Anzai T., Shina T., Kimura N., Yamagiya K., Kohara S., Shigenari A.,

Yamagara T., Kuleki J.K., Naruse T.K., Fujimori Y., Pukuzumi Y.,

Yamazaki M., Tashiro H., Iwamoto C., Umchara Y., Imanishi T.,

Meyer A., Ikeo K., Golobori T., Bahram S., Inoko H.;

"Comparative sequencing of human and chimpanzee MHC class I regions

unveils insertions/deletions as the major path to genomic
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface (By similarity).
SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNP-C) (Tumor necrosis factor ligand superfamily member 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuleki J.K., Shiina T., Anzai T., Kohara S., Inoko H.; "Comparative genomic analysis of the MHC: the evolution of class I duplication blocks, diversity and complexity from shark to man."; Immunol. Rev. 190:95-122(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                             DPGAQAQQGL -> GLSAPGSGRT (IN RBF.
                                                                                                                                                                                                                                                     Length 244;
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                                                                                                                                                                                                                          25390 MW; F41569459830ED4C CRC64;
                                          Missing (In isoform 2)
/FIId=VSP_006442.
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/FTId=VAR_016331.
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                                006441
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Prid=VAR 013026
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100.0%; Pred. No. 38;
ive 0; Mismatches
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MEDLINE=22381002; PubMed=12493009;
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15-WAR-2004 (Rel. 43, Last sequ
15-WAR-2004 (Rel. 43, Last anno
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Best Local Similarity luv...
7; Conservative
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Hydrolase; Metalloprotease; Zinc; Complete proteome

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                 EMBL; AB054536; BAB83801.1; -
R EMBL; AB100082; BAC78156.1; -
R InterPro; IPR006052; TWF family.
R InterPro; IPR006052; TWF family.
R InterPro; IPR00833; TWF-like.
R InterPro; IPR008365; TWF family.
R Pfam; PP00229; TWF; 1.
R Pfam; PP00229; TWF; 1.
R PRODO; PD00207; TWF subf; 1.
R PROSITE; PS00251; TWF ii. 1.
R PROSITE; PS0049; TWF 2; 1.
Cyrokine; Transmembrane; Glycoprotein; Signal-anchor.
Cyrokine; Transmembrane; Glycoprotein; Signal-anchor.
T TRANSMEM 19 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPACTOR: Binds I zinc ion per subunit (By similarity). SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Belongs to peptidase family M48.
                                                                                                                                                                                                           244 AA; 25420 MW; A4047858335D5B97 CRC64;
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                                                                                                                                                                                                                                                 DB 1; Length 244;
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NCBI_TaxID=63363;
                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update) 28-PEB-2003 (Rel. 41, Last annotation update) Probable protease htpX homolog (BC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; M48.004; -.
HAMAP; MF.00188; -.; 1.
InterPro; IPR006025; Pepti M. Zn. BS.
InterPro; IPR001915; Peptidase M48.
Pfam; PP01415; Peptidase M48; I.
PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
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                                                                                                                                                                                           (POTENTIAL).
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Pred. No.
 or send an email to license@isb-sib.ch
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                                                                                                                                                                                                                                                 2.3%;
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nes 7; Conservative
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222
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Aquifex aeolicus.
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067798;
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SEQUENCE FROM N.A.

ROWEN L., QIN S., Madan A., Abbasi N., James R., Dickhoff R.,

Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;

Sequence of the mouse major histocompatibility class III region.";

Submitted (OCT-1999) to the RMEL/GenBank/DDM databases.

-!- FUNCTION: Cytokine that binds to LTRE/THFRSP3. May play a specific

role in immune response regulation. Provides the membrane anchor

for the attachment of the heterotrimeric complex to the cell
                                                                                                                                                                                                                                                                                          Gaps
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
15-FEB-2003 (Rel. 41, Last annotation update)
15-FEB-2003 (Rel. 41, Last annotation update)
15-FEB-2003 (RINF-C) (Tumor necrosis factor (Tumor necrosis factor ligand superfamily member 3).
15-FEB-1995 (Rel. 31, Created)
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-1- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-1- SIMILARITY: Belongs to the tumor necrosis factor family.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
MRDLINE=9548660; PubMed=7846035;
Pokholok D.K., Maroulakou I.G., Kuprash D.V., Alimzhanov M.B.,
Kozlov B.V., Novobrantseva T.I., Turetskaya R.L., Green J.E.,
                                                                                                                                                                                                                                                                                          ö
                                                                                       (BY SIMILARITY)
                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                              Length 302;
                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                       INC (CATALYTIC) (BY SIMI)
3278BF481568E895 CRC64;
                                                      POTENTIAL.
ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
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                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AA
                                                                                                                                                                                                                              Score 7; DB 1
Pred. No. 46;
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                                 POTENTIAL
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STRAIN=C57BL/6; TISSUE=Spleen;
MBDLINE=95088371; PubMed=7995944;
                                                                                                                                                                           33030 MW;
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171
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27 1
151
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195 2
141 1
142 1
145 1
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P41155;
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us-09-524-531c-15.oli.rsp

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-!- FUNCTION: Cytokine that binds to LTBR/TNPRSF3. May play a specific role in immune response regulation. Provides the membrane anchor for the attachment of the heterotrimeric complex to the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arobom; Education TNF; 1.

PROSITE; PS00251; TNF 1; 1.

PROSITE; PS0049; TNP 2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

Cytokine; Transmembrane; Glycoprotein
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MEDLINE-20184748; PubMed=10721723;
Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
"Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes: structure, characterization and biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eurface.
-!-SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTA and one LTB subunits (By similarity).
-!-SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!-SIMILARITY: Belongs to the tumor necrosis factor family.
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28-FBB-2003 (Rel. 41, Created)
15-WAR-2003 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last sequence indicated in the constant of the consta
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Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 306 EXTRACELLULAR (POTENTIAL).
98 98 N-LINKED (GLCNAC. .) (POTENTIAL)
98 184 N-LINKED (GLCNAC. .) (POTENTIAL)
306 AA, 323328 MW, B7D276AB84A22549 CRC64;
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                                                                                                                                                                PIR; 149139; 149139.

MGD; MGI:104796; Ltb.

MGD; MGI:104796; Ltb.

INTERPORT: P:10mph gland development; IMP.

INTERPORT: IPRO06053; TNF family.

INTERPO: IPRO08093; TNF family.

INTERPO: IPRO08093; TNF like.

INTERPO: IPRO03056; TNF like.

PEAM: PF00229; TNF; 1.

PRINTS; PR01224; TNF; 1.

PRODOM: PD002012; TNF gubf; 1.

SMART; SM00207; TNF; 1.
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EMBL, U16984, AAB60493.1; -.
EMBL, U16985, AAAA70089.1; -.
EMBL, U06950, AAA18592.1; -.
EMBL, AF109719; AAC82483.1; -.
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CARBOHYD
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TNFC_MARMO
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                      (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

D -> H (IN REF. 1; AAF3465).

73B354EFC8B3B3BE CRC64;
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                                                                                                                                                                                                                                                                                                 Query Match

2.3%; Score 7; DB 1; Length 310;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                             Cytokine; Transmembrane; Glycoprotein; Signal-anchor. DOMAIN 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 15, 2004, 11:10:31
Job time : 11 secs
                                                                                                                                                      PROSITE, PS00251; TNF 1; FALSE NEG.
PROSITE, PS50049; TNF 2; 1.
                                              InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR008083; TNF gubf.
Pfam; PR01229; TNP; 1.
PRINTS; PR01224; TNF RECOSISPCT.
ProDom; PD002012; TNF gubf; 1.
SMART; SM00207; TNF; 1.
         EMBL; AF096268; AAF34866.1; -. EMBL; AF095587; AAF34865.1; -. HSSP; P01374; 1TNR.
                                                                                                                                                                                                                                                                           310 AA; 32644 MW;
                                                                                                                                                                                                                                   310
272
280
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                                                                                                                                                                                                                                                                                                                                                        252 VLAVLAL 258
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272
280
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2004, 11:05:50; Search time 36 Seconds

(without alignments)

2716.962 Million cell updates/sec
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Title: Perfect score: Sequence:	US-09-524-531C-15 310 1 MALRRPPRLALCARLPDFFLVNYIRTDEEGDFRHKSSFVI 310
Scoring table:	OLIGO Gapop 60.0 , Gapext 60.0
Searched:	1017041 seqs, 315518202 residues
Word size :	0

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Listing first 45 summaries

1017041

Total number of hits satisfying chosen parameters:

SPTREMBL 25:*	1: sp_archea:*	2: sp_bacteria:*	3: sp_fungi:*	4: sp human:*	5: sp_invertebrate:*	6: sp mammal:*	 gs :	d ds :	. sp	1: sp	12: sp virus:*	1 1	14: sp_unclassified:*	15: sp_rvirus:*	16: sp_bacteriap:*	17: sp_archeap:*
Database :																

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	***************************************	Q9bx67 homo sapien	OHOC	Q96fll homo sapien	Q9d8b7 mus musculu	Q9dim9 mus musculu	Q9epk4 mus musculu	Q8bt59 mus musculu	Q9tnt2 homo sapien	Q8hwg1 homo sapien	Q867wl procambarus	Q8i8al anopheles g	Q8c4v2 mus musculu	Q89e35 bradyrhizob	Q8tqt5 methanosarc		Q91r49 arabidopsis
	E	t	Q9BX67	QBWWLB	Q96FL1	Q9D8B7	Q9D1M9	Q9EPK4	Q8BT59	Q9TNT2	Q8HWG1	Q867W1	081851	08C4V2	Q89B35	Q8TQT5	Q8ZSR8	Q9LR49
	ä	3	. 4	4	4	11	11	11	Ħ	7	7	ß	ហ	11	, 16	17	17	10
	Query	Table 1	310	355	309	310	310	310	64	39	67	76	131	154	231	231	232	233
مد	Query	1000	100.0	100.0	67.1	10.3	0.6	9.0	4.2	5.6	5.6	5.6	5.6	2.6	2.6	5.6	5.6	2.6
	9	27020	310	310	208	32	28	28	13	<b>c</b> o	σο	60	8	8	80	80	80	60
	Result		7	7	m	4	S	9	7	80	σ,	10	11	12	13	14	15	16

Q966c0 caenorhabdi	Q98eq9 rhizobium l		Q9rpi7 desulfitoba	o	Q9mx15 pan troglod	Q9mwj9 gorilla gor	O9pr46 ureaplasma	Q95hc2 homo sapien		Q9xrx7 pongo pygma					obuod	pongo	homo	homo		pan		Þ	_	_		-	lactocc	Q9w6el gallue gall
039960	6 Q98EQ9	Q9N4Y9	Q9RPI7	0 Q9C7E9	Q9MXL5	ОЭММЭЭ	6 Q9PR46	Q95HC2	Q9XRX8	Q9XRX7	Q9MXG4	046684	Овинно	Q8MH11	QBMHG8	Q8MHG9	019617	Q860B0	Q852X8	Q9TPL2	Q9MKD2	Q7YQB2		6 Q8G5D2	6 Q8Z1U9	6 Q8BK37	6 Q9CIF4	3 Q9W6В1
246 5	294 1	309 5	322 2	336 1	338 7	348 7	348 1	363 7	365 7	365 7	365 7	366 6	366 7	366 7	366 7	366 7	366 7	366 7	366 7	366 7	366 7	366 7	449 1	452 1	492 1	659 1	784 1	1290 1
5.6	5.6	5.6	5.6	2.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	9.2	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	2.6	5.6	5.6
60	60	60	60	60	60	80	œ	<b>a</b> o	<b>a</b> 0	80	00	80	œ	æ	æ	æ	<b>6</b> 0	æ	60	œ	60	80	œ	œ	00	ω	œ	80
17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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SEQUENCE PROM N.A.
TISSUE-Eye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NIGGIIGGVLVVLAVLALITIGICCAYRRGYFINNKQDGBSYKNPGKPDGVNYIRTDBBG 300
241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGBSYKNPGKPDGVNYIRTDBBG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDPRIBWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                                10. SBOURNCE PROM N.A.
14. ISOGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
14. ISOGAI T., Ota T., Nishikawa T., Hayashi K., Cotsuki T., Salto K.,
14. Asuzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Salto K.,
15. Amanoto J., Wakamatsu A., Nakamura Y., Kojima S., Nasahari K.,
16. Amanoto J., Wakamatsu A., Nakamura Y., Kojima S., Sasaki N.,
17. Amanoto J., Okumura K., Iwayanagi T., Minomiya K.;
18. Amtori A., Okumura K., Iwayanagi T., Minomiya K.;
18. Amtori A., Okumura K., Iwayanagi T., Minomiya K.;
18. Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
18. EMBL; AR3448478; AAK27221.1; -.
18. EMBL; AR448478; AAM20925.1; -.
18. EMBL; AK073109; BAC11195.1; -.
18. EMBL; AK073109; BAC11195.1; -.
18. InterPro; IPR007110; Ig-like.
18. France France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDSRANPRPRNSSPHINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phillips H.M.; "Narrowing the critical region within 11q24-qter for hypoplastic left "Narrowing the critical of a candidate gene, JAM3, expressed during heart and identification of a candidate gene, JAM3, expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 310; DB 4; Length 310; Best Local Similarity 100.0%; Pred. No. 0; Matches 310; Conservative 0; Mismatches 0; Indels (
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL 1 30 POTENTIAL.
SECUENCE 310 AA; 35020 MW; CE39ADF33EA1DAB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Junction adhesion molecule 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Submitted (OCT-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDPRIEWKKIQDEQTTYVPPDNKIQGDLAGRABILGKTSLKIWNVTRRDSALYRCEVVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 MALRARPPRIRICARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFBSVELSCIITDSQT 105
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                   Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010690.1;
InterPro; 1PR007110; Ig-1ike.
InterPro; 1PR0047; ig; 2.
Fram; PR00407; ig; 2.
Fram; PR00407; ig; 2.
Frostre; PS50835; IG_LIKE; 2.
Hypothetical protein; Immunoglobulin domain.
NOW TER
SEQÜENCE 309 AA; 34917 MW; 50C5B1B7872E8DF3 CRC64;
                                                                                                                                                                                                                                                                                    JUNCTION ADHESION MOLECULE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
cardiogenesis.";
Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416101; CAC94776.1; -.
Genew, HGNC:15532; JAMJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR0047110; Ig-2.
Pfan; PF00647; ig; 2.
SMART; SM00408; IGc2; 1.
FROSITE; PS50835; IG_LIKE; 2.
FROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                    CHAIN 76 355 JUNCTION ADHESION MOLECUL SEQUENCE 355 AA; 39602 MW; 8B1577DEA7B1D4F8 CRC64;
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1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 310; D
100.0%; Pred. No. 0;
:ive 0; Mismatches
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Best Local Similarity 99.7
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Gaps

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Indels

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0; Mismatches

Conservative

32;

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Matches
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Q9D1M9
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STRAIN-C578 J6.5; TISSUB-Small intestine;

KADINE-21085660; PubMed-11217851;

KADINE-21085660; PubMed-11217851;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa T., Saito R.,

Alzawa T., Saito R.,

Balara T., Saito R.,

Radota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,

Ruhel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuhel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochrim L.M., Staubli F., Suviki R., Tomita M., Wagner L., Washio T.,

Baka J., Boffelli D., Bojinga N., Carninol P., Ge Bonaldo M.P.,

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Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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Lyons P., Marchionni L., Mashima J., Mazarelli J., Moabaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Milming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

"Punctional annotation of a full-length mouse cDNA collection.";
                                                            121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSHYRNDVPLP 180
                                                                                                                                                                                       241
                                                                                                                                                                                                         181 TDSRANPRFRANSFHLINSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240
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19
                  1 ALRRPPRIRICARLPDFFLLLFRGCLIGAVNLKSSNRTPVVQBFBSVELSCIITDSQTS
ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQBFBSVELSCIITDSQTS
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 5.4e-25;
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JCAM3 OR JCAM2 OR 1110002N23R1K.
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EMBL, AKO08187; BAB55519.1; -.
InterPro; IPR007110; Ig-11ke.
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100.0%;
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Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
Whithaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wasabi J., V.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Nature 409:685-690(2001).
Mature 409:685-690(2001).
InterPro; IPR001598; Ig_c2.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
JAM-3 OR JCAM-3 OR JCAM-2 OR J110002N23RIK.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
72
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41 PVVQEPESVELSCIITDSQTSDPRIEWKKIQD
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                 1110002N23Rik protein.
JCAM3 OR JCAM2 OR 1110002N23RIK.
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SMART; SM00408; IGC2; 1.
PROSTIE; PSS0835; IG_LIKE; 2.
Immuncglobulin domain.
SRQUENCE 310 AA; 34819 MW;
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SEQUENCE FROM N.A.
STRAINE-CSTBL/G0; IISSUE-Body;
MEDLINE-CSTBL/G1; IISSUE-Body;
The FANTOM Consortium,
The FANTOM Consortium,
The FANTOM Consortium,
The RAINTSU Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.;
Nature 420:563-573(2002).
BMBL; AX017692; BAC2526.1; -.
NON_TER
                                                           Junction cell adhesion molecule 3 (Pragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE-299110146; PubMed-9894855;
van dar Viles S., Voorter C., van den Berg-Loonen B.;
van dar Viles S., Voorter C., van den Berg-Loonen B.;
"A reliable and efficient high resolution typing method for HLA C using sequence-based typing.";
Tissue Antigens 52:558-568(1998).
EMBL; Y16418; CAA76206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRomo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buthoria; Primetes; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 13; DB 11; Length 64; 100.0%; Pred. No. 1.7e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE 64 AA; 6996 MW; AF46BC30AA6D0C11 CRC64;
              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 2.2
rative 0; Mismatches
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nes 13; Conservative
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SEXAIN=CS7BL/6J; TISSUB=Mesonephros;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
                                                                                               Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.; "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
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        Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Submitted {MAR-2002} to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
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Nature 420.563-573 (2002).
EMBL; AJ300304; CAC20704.1; .
EMBL; AK011156; BAB28663.1; .
EMBL; BC024357; AAH24357.1; .
EMBL; AK032833; BAC28049.1; .
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
The RELINES-213466B1;
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
TANALYRIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAS.";
Nature 420:563-573(2002).
EMBL; AK080981; BAC38104.1; -.
Bypothetical protein.
Xu P., Smith D.P.;
"Identification of distinct families of odorant-binding in the genome
of Anopheles gambiae.";
submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AY146791, AA012090.1;
GO; GO:0005819; P:odorant binding; IBA.
GO; GO:0005819; P:transport; IBA.
InterPro; IPROG170; PPF GOBP.
Pfam; PPF01995; PBP GOBP.
Pfam; PPF01995; PBP GOBP.
SEQUENCE 131 AA; 14884 WW; PC7D5289740B2A64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-USDA 110;
MEDLINE-22484998; PubMed-12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length 154;
                                                                                                                                                                                                                                                                                                                     Length 131;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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Local Similarity 100.0%; Pred. No. 8.2;
les 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 AA
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                                                                                                                                                                                                                                                                                                                  2.6%; Score 8; DB 5
100.0%; Pred. No. 7.1
rative 0; Mismatches
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Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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SEQUENCE 15
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Q8C4V2;
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ID Q89E35
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Q8C4V2
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Yasuda-Kamatani Y., Yasuda A.;
Yasuda-Kamatani Y., Yasuda A.;
"Cloning of cDNA for a neuropeptide precursor protein from Procambarus clarkii.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB036712; BAC55399.1;
EMBL; AB036713; BAC55390.1;
SEQUENCE 76 AA; 7895 WW; 3A3DF225947483AA CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Odorant-binding protein G.38B.a.
Anopheles gambiae (African malaria mosquito).
Bukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TAXID=7165;
                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-UIN-2003 (TrEMBLrel. 24, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide precursor protein.
Procambarus clarkii (Red swamp crayfish).
Bukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca; Bunalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
Astacoidea; Cambaridae; Procambarus.
NCBI_TaxID=6728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                              Delfino L., Morabito A., Ferrara G.B., "HLA-Cw+07012 sequence updating: from exon 6 to exon B." Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AA; 6538 MW; 543B57P5P97D7PF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%; Score 8; DB 7;
100.0%; Pred. No. 3.7;
iive 0; Mismatches
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EMBL; AY162382; AAN84536.1; JOINED.
EMBL; AY162383; AAN84536.1; JOINED.
EMBL; AY162384; AAN84536.1; JOINED.
NON TER
SEQÜENCE 67 AA; 6538 MW; 543857
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      MHC class I antigen (Pragment)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                            Homo sapiens (Human).
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                                                                                                                                                NCBI_TaxID=9606;
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Q818S1;
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10867W1
10 0867W1
AC 0867W
DT 01-JUD
DT 01-JUD
DT 01-JUD
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OS BUKARI
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OC RUMBILO
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Hypothetical protein PAB3614.
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SEQUENCE FROM N.A.

STRAIN=C2A / ATCC 35395 / DSM 2834;

KRELINE=21929760; DubMed=11932238;

KRELINE=21929760; DubMed=11932238;

KREINE-21929760; DubMed=11932238;

KREALINE-21929760; DubMed=11932238;

KREALINE-21929760; DubMed=11932238;

KREALINE-21929760; DubMed=11932238;

KREALINE-21929760; DubMed=21932238;

KREALINE-21929760; DubMed=219223;

KREALINE-21929760; DubMed=219223;

KREALINE-21929760; DubMed=219223;

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Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Res. 9:189-197(2002).
EMBL; AD005961; BAC52517.1; -.
GO; GO:0016021; C:integral to membrane; IRA.
InterPro; IPR004254; HlyIII_related.
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Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                        2.6%; Score 8; DB 16; Length 231;
100.0%; Pred. No. 12;
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SEQUENCE 231 AA; 25437 MM; 7AAB21CEE0B6500B CRC64;
                                                                                                                                                                                                                                 231 AA; 25052 MW; 254BB5B98D40D58B CRC64;
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Last annotation update)
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.00.0%; Pred. No. 12;
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Best Local Similarity 100.0%; Pred. No. 12,
Marches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                     0; Mismatches
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell surface lipoprotein.
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   249 VLVVLAVL 256
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SEQUENCE 231 AA
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Q8TQT5
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(TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)

01-MAR-2002 ( 01-MAR-2002 ( 01-JUN-2003 (

OSZSRB;

Q8ZSRB

**082SR8** 

232 AA.

PRT;

PRELIMINARY;

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OS Pyrobaculum aerophilum.

OC Archaea; Crenarchaeota; Thermoproteales;

OC Thermoproteaceae; Pyrobaculum.

OX NCBI TaxID=1373;

RN [1]

RP SEQUENCE FROM N.A.

RC STRATH=IM2, A ALCE 51768 / DSM 7523;

RA Miller J.H.;

RA Miller J.H.;

RA Miller J.H.;

RA Miller J.H.;

RY MEDLINE=21664397; PubMed=11792869;

RA Miller J.H.;

RY MEDLINE=21664397; PubMed=11792869;

RA Miller J.H.;

RY MEDLINE 2164397; PubMed=11792869;

RA Miller J.H.;

RY MEDLINE 2164397; PubMed=11792869;

RA Miller J.H.;

RY Machinum."

RY Alcoome sequence of the hyperthermophilic crenarchaeon Pyrobaculum

RT aerophilum."

RY Machiner J. Aalc5045.1; ---

DR REMBL, AR009941; Aalc5045.1; ---

DR REMBL, AR009941; Aalc5045.1; ---

DR REMBL, AR009941; Aalc5045.1; ---

SQ SRQUENCE 232 AA; 25942 MW; 39ASBECC4403P903 CRC64;

Query Match

SQ SRQUENCE 232 AA; 25942 MW; 39ASBECC4403P903 CRC64;

Authorized Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 17 DPFLILLE 24

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Search completed: June 15, 2004, 11:11:56

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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61 SDPRIEWKKIQDEOTITYVFFDNKIQGDLAGRAEILGKTSLKIWNTRRDSALYRCEVVAR 120
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PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 2001-07-12

PRIOR PILING DATE: 1309-07-28

PRIOR PILING DATE: 1399-07-07

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1399-07-28

PRIOR PLILING DATE: 1399-07-28

PRIOR PLILING DATE: 1399-07-28

PRIOR PLILING DATE: 1399-09-13

PRIOR PLILING DATE: 1399-10-05

PRIOR PLILING DATE: 1399-10-05

PRIOR PLILING DATE: 1399-11-29

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PRIOR PLILING DATE: 1399-12-02

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PRIOR PLILING DATE: 1399-12-06

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PRIOR PLILING DATE: 1399-12-07

PRIOR PRIOR PLING NUMBER: PCT/USS9/30919

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Roy, Margaret Ann
Stewart, Timothy A.
                                                                         Kljavin, Ivar J.
Mather, Jennie P
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            FRIOR APPLICATION NUMBER: PCT/USS9/23089
FRIOR PILING DATE: 1999-10-05
FRIOR PILING DATE: 1999-11-29
FRIOR PILING DATE: 1999-11-29
FRIOR PILING DATE: 1999-11-29
FRIOR PILING DATE: 1999-11-30
FRIOR PILING DATE: 1999-11-30
FRIOR PILING DATE: 1999-12-02
FRIOR PILING DATE: 1999-12-02
FRIOR APPLICATION NUMBER: PCT/USS9/28565
FRIOR PILING DATE: 1999-12-02
FRIOR PILING DATE: 1999-12-16
FRIOR PILING DATE: 1999-12-16
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FRIOR PILING DATE: 1090-12-20
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Patent No. 6664376
GENERAL INFORMATION:
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Gao, Wel-Clang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
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Filvaroff, Bllen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Matches 310; Conservative
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ORGANISM: Homo Sapien
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